Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name Art Unit:	Phone Number :	30	Examiner #:		Date:	· ·
Mail Box and Bldg/Ro	om Location:	Resi	Serial Nur	nber:	DADED DIC	E E V
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lease provide a detailed st nelude the elected species tility of the invention. De nown. Please attach a cop	fine any terms that may I	have a special w	iyms, and registry ni	ssible the subj imbers, and colles or relevan	ect matter to be a ombine with the o citations, author	earched. concept or s, etc, if
Title of Invention:					·	
nventors (please provide	full names):					
Earliest Priority Filing	Date:		· · · · · · · · · · · · · · · · · · ·		· · · ·	
*For Sequence Searches On						
ppropriate serial number.	у стологина ин реги	rem injormation (parent, child, division	ai, or issued pa	itent numbers) alo	ng with the
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STAFF USE ONLY	1	***********	********	****	*****	****
SEARCHERS TO WELL	17 h / Lu	Search		s and cost wh	ere applicable	
earcher Phone #: 308-9	NA Sequ	:ence (#)/	STN	<u> </u>	• • • • • • • • • • • • • • • • • • • •	

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Maximum Match 100%
Listing first 45 summaries
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5: gb_pl:
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12: gb_r:
13: gb_s:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6.1	6.2	6.3	6.3	6.3	7.5	8.6	9.1	9.1	9.1	9.1	100.0	Query Match
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M36700 E. coli iro	AE004272 Vibrio ch	U82598 Escherichia	AE000165 Escherich	M24142 E. coli iso	D90911 Synechocyst	X82644 P.aeruginos	AF008220 Bacillus	299119 Bacillus su	M74538 Bacillus su	M74521 Bacillus su	AF069740 Homo sapi	Description

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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Homo sapiens r
AF069740
AF069740.1 G1
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Submitted (03-JUN-1998) Pediatrics,
of Medicine, 600 N. Wolfe Street, Cl
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287-3654, USA
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mumalia; Eutheria; Primates;
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AIATAKTAQALQGAYVFGAQSFDEQEYPQSELMAGFWFVPEVMVTIAADKITFGSDTV
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M98048 Sulfolobus

Z50014 S.solfatari

AJ288281 Yersinia

AJ288282 Yersinia

AJ288282 Yersinia

AJ288282 Yersinia

AJ288284 Yersinia

AJ288285 Yersinia

V01378 Salmonella

J01812 s. typhimuri

AF030155 Drosophil

AC015023 Drosophil
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Y09356 Pseudomonas
M87483 L. lactis t
AE004162 Vibrio ch
U52150 Vibrio chol
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AF078080 Arabidops
AJ006065 Catharant
250849 E.coli menf
AE000316 Escherich
D90858 E.coli geno
U26444 Bacillus su
299120 Bacillus su
299120 Bacillus su
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D26185 B. subtilis
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AF022186 Cyanidium
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                                                                                                                                                                                                                     GTGGCTATGTCAGGTGGTCAGATCGCTACGGCGGCGGTCGCTGGGACAAGCCGGCGCGGG
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                                                                                                                                                                ACGGATGGCGCTGACGATATCGCGTTAGGCGAAGCGTTGTTAGCCAGTCAGAAAAAACCGC
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llarity 100.0%;
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LSDTLENQIIRALAEQANTYHVLKRHDELFISATPERLVAMSGGQIATAAVAQTSR
RGTDGADDIALGEALLASQKNRIERTGYVVASTITRLQDVTTSLKVPAMPSLLKN\DV
RTTDGADDIALALSVRAIVDRUHFTPALGGVPREAALYYIATHEKTPROLFAQFIGY
FTADNSGEFVVGIRSMYVNQTQRRATLFAGAGIVADSDAQQEYEETGLKFEPMRQLLK
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0; Mismatches
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RESULT 2
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Bacillus subtilis DNA.
Bacillus subtilis
Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Clostridium
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Bacillus subtilis menaquinone
M74521
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1 (bases 1 to 4000; 4001 to 5932)
Driscoll,J.R. and Taber,H.W.
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582. . 1547
                                                                                                                                                                                                                                                                                                           /gene=
142. .
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142. .5
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582. .1547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bacillus subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                             function="Message containing ORF1 to possibly ORF5"
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1624 . 2049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIGDLSFYHDLNGLLAAKKLGIPLTVILVNNDGGGIFSFLPQASEKTHFEDLFGTPTG
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/function="Convert isochorismate
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  316;
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/product="None"
4986. .5013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="menB"
/evidence=experimental
4975. .4982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4963
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/note="putative"
4157. .4942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKIFDETYNGIAKITINRPEVHNAFTPKTVAEMIDAFADARDDQ
NVGVIVAGAGDKAFCSGGDQKVRGHGGYVKDDQIPRLNVLDLQKIIRVIPKFVVAMV
SGYAIGGGHVHIVCDLTIAADNAIFGQTGFKVGSFDAKYGSGYLARTVGHKKAREN
YLCRQYNAQEALDMGLVNTVVPLEQLEEETIKWCEEMLEKSPTALRFIKAAFNADTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="dihydroxynapthoic
/protein_id="AAA50401.1"
/db_xref="GI:557492"
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4148. .4152
                                                                                                                                                                                   biosynthesis."
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5038. .>5932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="possible stabilized structure."
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                                                                                                                                                                                                                               /standard_name="MenE"
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/function="possible stabilized of RNA secondary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAGIQQFAGDATLLYYTTDEAKEGRDSFKEKRKPDFGQFPRFP"
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/standard_name="Men
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060. .5722
                                                                                                                                                                                                                                                                                                                        'evidence=experimental
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Tuerk,C., Gauss,P.,
Stormo,G., d'Aubent
Brody,E.N. and Gold
                                                                                                                                                                                                                                                                             Bactilus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Clostridium
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M74538 M74182 M74183
M74538.1 GI:1185287
                                                                       92332443
                                                                                                          operon
                                                                                                                         Bacillus subtilis J. Bacteriol. 170 (6),
                                                                                                                                                                                                                             Miller, P., Mueller, J., Hill, K. and Taber, H. Transcriptional regulation of a promoter in
                                                                                                                                                                                                                                                                                                                                                                                                                          BACMENAQOP 5946 bp
Bacillus subtilis me
                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group;
1 (bases 1 to 5946)
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 Gauss,P., Thermes,C., Groebe,D.R., Gayle,M., Gui
d'Aubenton-Carafa,Y., Uhlenbeck,O.C., Tinoco,I.
and Gold,L.
                                                                                         174
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Location/Qualifiers

1. 5946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rowland, B., Hill, K., Miller, P., Driscoll, J. and Taber, H. Structural organization of a Bacillus subtilis operon encoding menaquinone biosynthetic enzymes Gene 167 (1-2), 105-109 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUUCGG hairpins: extraordinarily stable RNA secondary structures associated with various biochemical processes Proc. Natl. Acad. Sci. U.S.A. 85 (5), 1364-1368 (1988)
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/note="5'
                                                                                                                                                                                                                                                                                                                                                                                   CSEVEKPDGPVLYKTKSVQHLFTPIVGQLRESASIFDLIEKLHPTPALGGSPQEKAVD
VIREIEPMSRGWYAAPIGWIDSQDNGEFAVAIRSGLIEGSTARLFAGCGIVEDSEPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MVTTVQRTFRKEVLHALHKAKEVNHAVLISYSRQIESLDPLSFF
NYGAKKYTGNRFFWSDPESELTIVGLGKEAVFQTNQKNSERYREVFEQWERFKKTAFH
IYEEEKLQHSAVGPVLFGGFSFDPCEERGSQWDHFSEGDFFVPALMLTWTAEGFFLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="based on similarity to AmoA, B. subtilis DhbC"
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/citation=[1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclea:
1988);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="regulatory site 14...19
                 /translation="MTVNPITHYIGSFIDEFALSGITDAVVCPGSRSTPLAVLCAAHP
DISVHVQIDERSAGFFALGLAKAKQRPVLLICTSGTAAANFYPAVVEAHYSRVPIIVL
                                                         carboxylate synthase"
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/db_xref="GI:1185289"
                                                                                                                                                                                                           /gene="menD"
/note="based on similarity to
                                                                                                                                                                                                                                                                                                                                           1541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="isochorismate synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="menf"
/note="based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="menF"
143. .1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bacillus subtilis"
/strain="RB1"
                                                                                                                                                                                           analysis of mutants
                                                                                                                                                                                                                                                                                                 /gene="menD"
1541. .1545
                                                                                                                                                                                                                                                                                                                                                                 EYEETQIKLKPMISALGGERR"
                                                                                                                                                                                                                                                                                                                                                                                                                                              IKEKQYDKVVLARELLLTFDGPIQIEPVLKTLLDDQQTSYVFAIEQEGKTFVGASPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRWVSGGEDAEAVLEGLKAFAAEFMVPDFKQEDQAVIAAAEELDKDDWLKAIETATSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence≃experimental
130. .134
TADRPHELRRVGAPQAINQHFLFGNFVKFFTDSALPEESPQMLRYIRTLPSRAAGEAQ
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                                                                                                                                                                     /codon_start=1
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1555. .3201
                                                                                                                                                                                                                                                                                                                                                                                                                             LIKRDGGTVMSSCLAGSIKRGVNEEDDRRIGLELLNDEKNLLEHDIVVGMIHNAFVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /citation=[1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1423"
                                                                                                                                               transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         te="5' RNA terminus mapped by high-resolution S1 lease protection assays (J. Bacteriol. 170, 2742-2748, 8); exact 3' terminus unclear, but transcripts into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are undetectable; contains ORF1 to possible ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1558
                                                                                                                                                                                         (J.
                                                                                                                                                                                       ity to E. coli MenD and enzymatic Bacteriol. 176, 2648-2653, 1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for pH regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli EntC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                 terminator
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4139. .4144
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3284. .3871
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4977. . .5007
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                                                                                                                                                                                                                                 /function="convert OSB-CoA
biosynthesis"
                                                                                                                                                                                                                                                                                                                                      /note="predicted MW estimated pI= 5.99"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="5' RNA terminus mapped by high resolution primer
extension assays.; Exact 3' terminus is unclear but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /citation=[2]
4152. .>5736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoters"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     menB RNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="sequence motif seen
B. subtilis genes involved
transport; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4103. .4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGTVNITVSDGVRYAVADEGPNASEAVVCLHGFTGSKQSWTFLDEMLPDSLIKLDCLGHGETDAFLNGKRYSTTRQVSDLAEIFDQLKLHKVKLIGYSMGGRLAYSFAMTYPSGGYBHLCLKARRRGSKHLLGNGGNESCGTGSLLILFYETGSKRLLRIGRISLCFHLSRGWLKIFGTGYDRAVCGTIRLGLRTV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVPENSSLFVGNSMPIRDVDTFFEKQDRPFRIYSNRGANGIDGVVSSAMGVCEGTKAP
VTLVIGDLSFYHDLNGLLAAKKLGIPLTVILVNNDGGGIFSFLPQASEKTHFEDLFGT
PTGLDFKHAAALYGGTYSCPASWDEFKTAYARRQTSPDSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDELKRKLRPDVVIRFGPMPVSKPVFLWLKDDPTIQQIVIDEDGGWRDPTQASAHMIH
CNASVFAEEIMAGLTAATRSSEWLEKWQFVNGRFREHLQTISSEDVSFEGNLYRILQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRPMGPVHVNVPLREPLMPDLSDEPFGRMRTGRHVSVKTGTQSVDRESLSDVAEMLAE
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                                                                                                                                                                                                                                                                                                                                                                                                       4171. .4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4162.
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                                                                                                                                                                                                                                                                                                                                                                                  /gene="menB"
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative"
/citation=[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /phenotype="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /citation=[2]
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                                                                                                                                                                                                             /evidence=experimental
                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                      /citation=[
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="menB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:143185"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 menB transcripts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 3871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by appropriate spacing from mapped
logy to B. subtilis vegetative type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triacylglycerol lipase of P. immobilis"
                                                                                                                                                                                                                                                                                                                                                              of 28584.4 Daltons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΡH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        menE."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                          acid (DHNA) synthetase"
                                                                                                                                                                                                                                                     DHNA in
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                                                                                                                                                                                                                                                       menaquinone
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                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from mapped 5'
                                                                                                                                                                                                                                                                                                                                                              a.a.
                                                                                                                                                                                                                                                                                                                                                              residues,
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Query Match
Best Local Similarity
Matches 316; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 TAGCTGAGCAGGCGAATACGTATCATGTGGTTTTAAAGCGACATGATGAATTGTTTATTT 580
                                                                                                                                                                                                                                                                                                                   CGATTGTTGACCGCTTGCATCCAACACCAGCACTGGGTGGCTCCCACGTGAAGCGGCCC 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGCCAGTCAGAAAAACCGCATTGAACATCAATATGTCGTGGCAAGTATCACGACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGACAAGCCGGCGGGGACGGATGGCGCTGACGATATCGCGTTAGGCGAAGCGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCGGCGGTCG
                                             AAACGCAGCGACGAGCAACTTTATTTGCTGGTGCCGGGATTGTGGCTGACTCCGATGCGC 1120
                                                                                                                                                                                                                        TGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGTTTGCAGGTCCTATTGGCT 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTTCAGCATTTGTACACCAACTTACAGGGGACATTGCGGCACATTTAAGTGTGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGCTCCATTAAACGAGGCGTGAATGAAGAAGACGACCGCCGGATAGGCCTTGAATTAT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGACGATCAGCAGACAAGCTATGTTTTTGCAATTGAACAAGAAGGCAAAACCTTTGTCG 953
                                                                                                                                             TTGACGTGATCAGGGAGATTGAACCGATGTCCCGCGGCTGGTATGCGGCCCCTATCGGCT
                                                                                                                                                                                                                                                                                       ACTTAATTGAGAAGCTGCACCCCACTCCCGCGCTTGGGGGATCACCTCAGGAAAAAAGCTG 1313
                                                                                                                                                                                                                                                                                                                                                                                       GCGTTCAGCACCTGTTTACGCCGATTGTCGGACAGCTGCGCGAGTCTGCTTCGATTTTTG 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTATCAAGCTGTTCAGAGGTTGAAAAGCCTGATGGACCTGTTTTGTACAAAACAAAAA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAAGACGTGACGACGTCGCTAAAGGTGCCGGCCATGCCAAGTTTACTCAAAAATAAGC 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.1%;
nilarity 49.3%;
Conservative
-GCACAGCAAGGCTGTTTGCCGGGTGCGGTATTGTGGAAGACTCGGAACCAA 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="menE"
/citation=[2]
5038..5043
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5000. .5027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Standard_name="'Golden Loop' sequence"
/note="sequence is very similar to that shown by Tuerk et
al [Proc. Natl. Acad. Sci. U.S.A. 85, 1364-1368 (1988)] to
confer stability to RNA stem-loop structures."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental 4989. .4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="possible stabilization of RNA secondary
structure"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stability (see misc.
/citation=[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="menE"
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5000. .5946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 108.6; DB 2;
Pred. No. 2.1e-22;
D; Mismatches 319;
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밁 Ş В δÃ 망 δÃ 망 δ 밁 ρy 밁 Q В Ş В Ş B Š 밁

CDS

complement (99. .1001)

/gene="ytnM"

/gene="ytnM" /function="unknown"

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REFERENCE
AUTHORS
TITLE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
BSUB0016/c
LOCUS
                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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          terminator
                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE 1 (bases 1 to 215640)

RS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Bzusedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Bzusedo, V., Bertero, M.G., Bersieres, P., Bolotin, A., Borchert, S., Bzusedo, V., Cadwell, B., Capuano, V., Canter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Daniel, R.A., Chim, S.Y., Claser, P., Goffeau, A., Golightly, E.J., Galizzi, A., Galiger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galightly, E.J., Galizot, M., Golightly, E.J., Galizot, M., Golightly, E.J., Galizzi, A., Galightly, E.J., Karamata, D., Kasahara, Y., Kohlen, J., Kumano, M., Kurita, K., Labidus, A., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Meltado, R.P., Mizuno, M., Moestl, C., Medigue, C., Medina, N., Mellado, R.P., Purnelle, B., Rapoport, G., Rey, M., Sadaie, Y., Sato, T., Sekowska, A., Seror, S., Nobeck, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Persecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Sadaie, Y., Sato, T., Sekowska, A., Seror, S., Schroeter, R., Sodfone, F., Setguchi, J., Sekowska, A., Seror, S., Serror, P., Shin, B.S., Soldo, B., Soldo, B., Takagi, T., Takahashi, H., Takemaru, K., Yasanotti, A., Winters, P., Walsanoto, H.
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                                                                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
Submitted (16-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete genome sequence of the gram-positive bacterium, Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis
to 3213410.
Z99119 AL009126
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.1 GI:2635411
complement(8. .24)
                                                                    complement(8. .1001)
                                                                                                           /strain="168"
/db_xref="taxon:1423"
                                       /gene="ytnM"
                                                                                                                                                                                  /organism="Bacillus subtilis"
                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                     /translation="MTRADFIOFGAMIHGVGGTTDGWRHPDVDPSASTNIEFYMKKAQ
TAEKGLESFIFIADGLFISEKSIPHFLKRFEPTTLESALASVTKNIGLVGTFSYSFTE
PTISRQLMSLDHISGGRAGWMLVTSPQEGARAHNSKKIPEHTERYEIAQEHLDVYG
GLWNSWEHDAFIHNKKTGQFFDQAKLHKLNHKGKYFQVEGPLNIGGSKGGEPVVFQAG
SSETGROFAAKNADAIFTHSNSLEETKAFYADVKSRADEGRDPSSVRIFPGISPIVA
DTEEBAEKKYREFAELIPIENAVTYLARFFDDYDLSVYPLDEPFPDIGDVGKNAFQST
TDRIKREAKARNLTLREVAQEMAFPRTLFIGTPERVASLIETWRNAEAADGFIVGSDI
GGTLDAFVEKVIPILQERGLYRQDYRGGTLRENLGLGIPQHQSVLHSSHH"
/gene="ytni"
complement(4352..4633)
/gene="ytni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2288. .2980)
/gene="ribR"
complement(2288. .2980)
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DIDALPIEEKTGLPYASKHKGIMHACGHDFHTAALLGAAFLLKENQDSLKGKTRLLFQ
PAEEAGAGATKVIEDGGLDAYIGLHNKPDIAGGTGKTGPLMAAVDRFKVEIEG
KGAHAALPHNGFDPIIGASQLIVALQTIVSRNVNPLQSAILTYGKINGGSTMNVIPDT
VVIEGTVRTFDSEVRNQVKQRFFAVTEQISAAFSLKANVKWHSGPPPLCNDEAITGLV
RDAAHKAKLQVIDPAPSTAGEDFAYYLEHIPGSFAFFGTDGDHDWHHPAFTIDETAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ytnJ" complement(3027. .4355)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNVIDNWFFEYGITQVAYRRIYILSFLSFLKEDNPKVSSKYIRFGAGGLADKLNRFIS
SYVEESEENILG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTIIAGTVVKGKQLGRKLGFPTANVDAKIHGLRNGVYGVLATVN
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SLTKQIKKDISCVAKRFELIGIMAPNKKESLLSHQELNLPDLCFYKKCNNLYGVNRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="transcriptional
/protein_id="CAB14908.1"
/db_xref="GI:2635414"
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complement(1020. .2270)
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LFVLSKIGNRNIVKTAVDVHLKEK"
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ASVHLAEVVTTAASGVSHIKFGNVDKGTVYQLVIPGSIGAFLGALFGALSQLEGDVAKPY
ISLFLLLLGGYVLIRFLFQYKPALEKKHVPLMKKQSIPLGVIAGFADAFGGGGGGVFT
TPILLSRKGLSPRKVVGTVDTSEFAIAVSATAGFLISLGWEDVNWLWVFSLMAGGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB14909.1"
/db_xref="GI:2635415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to nitrilotriacetate monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="regulation of riboflavin biosynthesis genes"
/note="alternate gene name: ytnK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KASYFLYESAKRLLDSNEESKISD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ytnJ"
/function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3027. .4355)
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/db_xref="GI:2635413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1020. .2270)
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                                                                                      /function="unknown"
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Best Local :
154216 GCGCGTCTCCGGAAAGACTGATCAAAAGAGACGGCGCACTGTCATGTCTTCCTGTCTGG 154157
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                                                 581 CAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCGGCGGTCG 640 '
                                                                                                                                                  521 TAGCTGAGCAGGCGAATACGTATCATGTGGTTTTAAAGCGACATGATGAATTGTTTATTT,580
                                                                                                                                                                                                                             Local Similarity
                                                                                                TGGACGATCAGCAGACAAGCTATGTTTTTGCAATTGAACAAGAAGGCAAAACCTTTGTCG 154217
                                                                                                                                                                                                        316;
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:034931"
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/translation="MQFDFPFIVSAMKEMVKTIPLTLMMAVLPIVFGFLVALGNIIVR
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FVYMALSLTAGAYLTBIIRSGILAMDTGQVEAAYSIGLTYSQTFRRVILPQALKVSIP
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	AF008220 AF008220 220060 bp DNA BCT 04-FEB-1998 DEFINITION Bacillus subtilis rrnB-dnaB genomic region. ACCESSION AF008220 VERSION AF008220.1 GI:2293135 KEYWORDS Bacillus subtilis. ORGANISM Bacillus subtilis. Bacteria, Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. REFERENCE 1 (bases 1 to 7430) AUTHORS Green,C.J., Stewart,G.C., Hollis,M.A., Vold,B.S. and Bott,K.F. TITLE Nucleotide sequence of the Bacillus subtilis ribosomal RNA operon, MEDLINE 86031361 MEDLINE 86031361 ACCESSION 04-FEB-1998 BCT 04-FEB	Db 153856 TTGACGTGATCAGGGAGATTGAACCGATGTCCGCGGCTGGTATGCGGCCCCTTATCGGCT 153797 Qy 1001 ATTTTACCGCAGATAATAGTGGGGAATTTGTGGTTGGCATCGGTTCCATGTATGT	Qy 641 CTGGGACAAGCCGGCGGGACGATGGCGTGACGATATCGCGTTAAGCGTATTGTTTTTTTT
REFERENCE 14 (bases AUTHORS Abe, A, K AUTHORS ABCALL MICROBIOLINE 95400496 REFERENCE 15 (bases AUTHORS KOZLOV, Y. TITLE Bacillus Bacillus JOURNAL MICROBIOLINE 96118703 REFERENCE AUTHORS ROWLAND, BUILT BACKBOOK AUTHORS Gene 167 MEDLINE Gene 167 MEDLINE 96144257		MEDLINE 9213624 REFERENCE 9 (bases AUTHORS PUTZET, H. TITLE CO-ordina Bacillus INVOLVING JOURNAL EMBO J: 1 MEDLINE 92347349 REFERENCE 10 (bases AUTHORS TITLE Identific acetoin in JOURNAL MO1. Micro MEDLINE 95020526 REFERENCE 11 (bases AUTHORS GRINDY, F.	Sell Nucki Nucki Nucki Nucki Nucki Sell Nucki Sell Nucki Sell Nucki Sell Nucki Sell Nucki
14 (bases 16985 to 19588) Abe,A., Koide,H., Kohno,T. and Watabe,K. A Bacillus subtilis spore coat polypeptide gene, cotS Microbiology 141 (Pt 6), 1433-1442 (1995) 95400496 15 (bases 131934 to 133970) Bolotin,A., Khazak,V., Stoynova,N., Ratmanova,K., Yomanta,Y. and Kozlov,Y. Identical amino acid sequence of the aroA(G) gene product of Bacillus subtilis 168 and B. subtilis Marburg strain Microbiology 141 (Pt 9), 2219-2222 (1995) 96118703 16 (bases 2558 to 31212) 17 (bases 2558 to 31212) 18 (bases 2558 to 31212) 19 (bases 2558 to 31212) 19 (bases 2558 to 31212) 10 (bases 2558 to 31212) 11 (bases 2558 to 31212) 12 (bases 2558 to 31212) 13 (bases 2558 to 31212) 14 (bases 2558 to 31212) 15 (bases 2558 to 31212) 16 (bases 2558 to 31212) 26 (bases 2558 to 31212) 27 (bases 2558 to 31212) 28 (bases 2558 to 31212) 29 (bases 2558 to 31212) 31 (bases 2558 to 31212) 32 (bases 2558 to 31212) 33 (bases 2558 to 31212) 34 (bases 2558 to 31212) 35 (bases 2558 to 31212) 36 (bases 2558 to 31212) 37 (bases 2558 to 31212) 38 (bases 2558 to 31212) 39 (bases 2558 to 31212) 30 (bases 2558 to 31212) 31 (bases 2558 to 31212) 32 (bases 2558 to 31212) 33 (bases 2558 to 31212) 34 (bases 2558 to 31212) 35 (bases 2558 to 31212) 36 (bases 2558 to 31212) 36 (bases 2558 to 31212) 37 (bases 2558 to 31212) 39 (bases 2558 to 31212) 30 (bases 2558 to 31212) 31 (bases 2558 to 31212) 32 (bases 2558 to 31212) 33 (bases 2558 to 31212) 34 (bases 2558 to 31212) 35 (bases 2558 to 31212) 36 (bases 2558 to 31212) 36 (bases 2558 to 31212) 37 (bases 2558 to 31212) 38 (bases 2558 to 31212) 39 (bases 2558 to 31212) 30 (bases 2558 to 31212) 31 (bases 2558 to 31212) 32 (bases 2558 to 31212) 33 (bases 2558 to 31212) 34 (bases 2558 to 31212) 35 (bases 2558 to 31212) 36 (bases 2558 to 31212) 37 (bases 2558 to 31212) 38 (bases 2558 to 31212) 39 (bases 2558 to 31212) 30 (bases 2558 to 31212) 31 (bases 2558 to 31212) 32 (bases 2558 to 31212) 33 (bases 2558 to 31212) 34 (bases 2558 to 31212) 35 (ba	the Bacillus subtilis; 175 (22), 7348-7355 (11 to 15526) tis,J.M., Beldman,G. and cillus subtilis: molecullus subt	92138624 92138624 92138624 92138624 92138624 11., Gendron,N. and Grunberg-Manago,M. Putzer,H., Gendron,N. and Grunberg-Manago,M. Co-ordinate expression of the two threonyl-tRNA synthetas genes Bacillus subtilis: control by transcriptional antitermination involving a conserved regulatory sequence EMBO J. 11 (8), 3117-3127 (1992) 92347349 10 (bases 134990 to 141290) 10 (bases 134990 to 141290) 11 (bases 134990 to 141290) 12 (control of genes involved in utilization of acetate and acetoin in Bacillus subtilis Mol. Microbiol. 10 (2), 259-271 (1993) 95020526 11 (bases 162129 to 164080)	5 (bases 201234 to 203212) Seki,T., Yoshikawa,H., Takahashi,H. and Saito,H. Nucleotide sequence of the Bacillus subtilis phoR gene J. Bacteriol. 170 (12), 5935-5938 (1988) 89053932 6 (bases 142232 to 144147) Grundy,F.J. and Henkin,T.M. Cloning and analysis of the Bacillus subtilis rpsD gene, encodi ribosomal protein S4 J. Bacteriol. 172 (11), 6372-6379 (1990) 91035248 J. Bacteriol. 172 (11), 6372-6379 (1990) 91035248 J. Bacteriol. 172 (11), Nicholson,W.L. and Chambliss,G.H. Catabolite repression of alpha-amylase gene expression in Bacil subtilis involves a trans-acting gene product homologous to the Escherichia coli laci and galk repressors Mol. Microbiol. 5 (3), 575-584 (1991) 91260441 8 (bases 140810 to 142610) Henkin,T.M., Glass,B.L. and Grundy,F.J. Nallysis of the Bacillus subtilis tyrS gene: conservation of a regulatory sequence in multiple tRNA synthetase genes

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Bacillus subtilis operon under the dual control of the general stress transcription factor sigma B and the sporulation transcription factor sigma H
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Submitted (13-JNN-1997) Laboratoire de Genetique Microbienne,
Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
Location/Qualifiers
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TCTCGGAATATGAAGAAACACAGATTAAATTGAAGCCGATG
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/product="tRNA-Ala"
6172. .6248
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/product="tRNA-Met"
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/product="tRNA-Ser"
6443. .6519
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/product="tRNA-Asp"
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/product="tRNA-Pro"
6079. .6151
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/product="tRNA-Ile"
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97136628
3 (bases
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Direct Submission
Submitted (27-SEP-1996) L. Serino, Universit
Biologie Microbienne, Batiment de Biologie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
Pseudomonas aeruginosa
Bacteria. n-----
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On Oct 23,
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Revised by [4]
4 (bases 1 to 4662)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (14-NOV-1994) L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biosynthesis of pyochelin and dihydroaeruginoic acid
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96086939
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X82644
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J. Bacteriol. 179 (1), 248-257 (1997)
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                                                                                                                                                                                      /transl_table=11
/protein_id="CAA57966.1"
/db_xref="G1:1628426"
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/note="similarity
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/db_xref="taxon:287"
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Location/Qualifiers
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)oin(256. .260,265. .1905)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1) L. Serino, University of Lausanne, Lab de Batiment de Biologie, 1015 Lausanne-Dorigny,
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/codon_start=1
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/protein_id="CAA57968.1"
/db_xref="GI:929779"
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/gene="pchB"
2651. .2959
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PLQVFGAWDDRQTPCLYWEQPELAFFANGCALELQGHGSQRFARI EENWQLLCADAVV
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EGPLAPRLCGGFRFDRGPREHWQAFADASLMLAGITVLREGERYRVLCQHLAKPG
DALALAAYHCSALLRLRQPARRRPSGFTAGAQGDASAQERQWFAKVSDAVSSVEQGR
FGKVVLARTQARPLGDIEPWQVIEHLRLQHADAQLFACRGNACFLGASPERLVRIRA
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PDAPGLKRLARVQHLNTPIRARLADAGGILRLLQALHPTPAVGGYPRSAALDYIRQHE
GMDRGWYAAPLGWLDGEGNGDELVALRSALLTPGRGYLFAGCGLVGDSEPAHEYRETC
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2956. .4386
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2651. .2959
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LLALQYPGREDRfneapatrledLadgaalalrdfadaplalfghSlgaalayetalr
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                                                     superoxide dismutase; tRNA delta-2-isopentenylpyrophosphate (IPP) transferase; tRNA-Gly; tRNA-Phe; transposase.
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3-isopropylmalate dehydrogenase;
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sp. (strain:PCC6803)
sp.
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1576593-1719643.
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Submitted (28-JUN-1996) to the DDBJ/EMBL/GenBank databases. Satoshi Tabata, Kazusa DNA Research Institite, Laboratory of Gene Structure 2: 1523-3, Yanauchino, Kisarazu, Chiba 292, Japan (E-mail:tabata@kazusa.or.jp, Tel:+81-438-52-3933,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A., Yamada, M., Yasuda, M. and Tabata, S. Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miyajima,N., Hirosawa,M., Sugiura,M., Sasamoto,S., Kimura,T., Hosouchi,T., Matsuno,A., Muraki,A., Nakazaki,N., Naruo,K., Okumura,S., Shimpo,S., Tabeta,G., Wada,T., Watanabe,A., Vanda, M. A., Tabeta,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential protein coding regions were assigned on the similarity search of the ORFs and GeneMark analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:+81-438-52-3934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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PDRRĒKLVQDĒNVQNKGDVĒTĒYGDKKOLVQNLLESFOQRĒDLESĪ (ZITMA I KRĄRQE
IPQVYLLVĢHGELPLAINEPRGI STAVTĀLENLGVTVQPLNVYTDGG I PĒDADAVVĪAG
PTRKĒLAPĒ I ATLKQYTDQGGNLLVMVS PĒADĀGLĒDLLĒPWĢVSĒDPRLV I DLSGAG
GVEGLDPTVP I FURYGNHP I TOKLĢGA IA I FELVRPVAT KEÇEHI QATTLVĒASDLMY
ATQLISĒDLQPNĒTDLLGPFDVAVALTREGKEVSSAKĒMETGNUTĒPĒBĒ INVSPSPAV
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                                                                                                                                        ARNTEAKAIWDAVERYGEMLVFEKERISQEWNQVSKNILSEDRKNTKNLEEDIEHI
                                                                                                                                                                                                                                                                                                                                                                 LPDLPIISLVEY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start-
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5614. . 6606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNTYTYGIISALGRSSSEVGYPDKRYRFIQTDAAINPGNSGGPLLNAKGEVIGVNTAI
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/note="ORF_ID:sll1427"
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translation="MWDNGSVRHLPRLIMRLSQMLFVTLRDDPADAEIPSHKLLVRAG"
                                                                                                                        transl_table=11
                                                                                                                                                           /codon_start=1
                                                                                                                                                                               note="ORF_ID:s111425"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCGCCAATTGGGGCAAGAGTTATTGCACAATCCCAAGGAATTGCGGGGAACATCAAGCG 128772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAACAGCTGGTCACCGATGCCCTAGCAGGTTCGGCTCCTAGGGATGTCCATGTCCAGGGC 128712
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ACTCTCTGGCGTTCTTTGA 129202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTTGGATTACCTCCAGCGTCTCCGGGCATTGGGCCTAAGCCCCCAGGCTTCCTCC 128832
                                                                                                                                                         GGGATTGTGGCTGACTCCGATGCGCAACAAGAATATGAAGAAACTGGGTTGAAATTTGAA 1155
                                                                                                                                                                                                                                                      GGTATTCGTTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTTGTTTGCAGGTCCTATTGGCTATTTTACCGCAGATAATAGTGGGGAATTTGTGGTT 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTGGCGTCCCACGTGAAGCGGCCCTGTATTACATTGCGACCCATGAGAAGACACCTCGT 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCCGCCCCACATCCCATCCCCTGGCCCTGGTGCAACAACTCCATCCCACCCCCGCTGTG
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                                                            CCCATGCGGCAATTGTTAA 1174
                                                                                                                        GGCATTGTGGCCGGTTCCGATCCCCTCAAAGAAGTGGCAGAAATTGAGCTCAAACTTCAA 129183
                                                                                                                                                                                                                                                                                                                  GGCATCCGTTCCATGTATGTGAATCAAACGCAGCGACGAGCAACTTTATTTGCTGGTGCC 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGGTGTCCCCGTAGCGATCGCCGAAGATTTAATCCGTCGCCATGAAACCTTTGACCGC 129009
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NLTEVATYALNRLPPLYASSVKGVEEQRRVAARQYRSELTSAVRRAIAAVERDPLRSS
EPIVSEIEVNYRGAENTLGQIQELLKRYNLLEPVNKEVTWDNCLPLLRQAFLKLTAVQ
SPTPPAINERRSMPLPPPPIRTPAMDNRQIDPKNTLM"
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IEVGHIFQLGTKYSQAMGATFTNEQGEEKPLVMGCYGIGVSRLAQAAVEQSYDKDGII
WPTAIAPYEVVIVVPNVGDEEQMQVAEQIYTEFQAAEVDVLLDDRNERAGVKFKDSEL
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ATIAKMCQCLDCDASNVVKNYLYQAVYNSGKAVLVLVSIRGDQEVNEVKLTNELTKLA
PHYESTNILSLTVPDEKEQQKWAAKPLPLGYISPGISDDYIATNKQVADKFLRLVDQT
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/protein_id="BAA18009.1"
/db_xref="GI:1653093"
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RPRFGLMRGREFIMKDAYSFHSDEASLKATYGAMDQAYRNIFSRCGLDFRPVDADSGA
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                                                                                                                                                                                                                                                              CAAGTATCACGACACGCTTGCAAGACGTGACGACGTCGCTAAAGGTGCCGGCCATGCCAA
                                                                                                                                                                                                                                                                                                                   AAGCAGGTAATCGTCTGCTGGCGTCAGAAAAAGATCGCCATGAACATGAACTGGTGACTC 1118
                                                                                                                  CACATTTAAGTGTGACCGCGATTGTTGACCGCTTGCATCCAACACCAGCACTGGGTGGCG
                                                                                                                                                         AGCTGATCACCACGCCGACGCTGTGGCATCTCGCAACTCCCTTTGAAGGTAAAGCGAATT 1238
                                                                                                                                                                                              GTTTACTCAAAATAAGCAAGTTCAGCATTTGTACACCAATTACAGGGGACATTGCGG
                                                                                                                                                                                                                                                                                                                                                      CGTTAGGCGAAGCGTTGTTAGCCAGTCAGAAAAACCGCATTGAACATCAATATGTCGTGG
                                                                                                                                                                                                                                                                                                                                                                                               TTAGCTCCATTCCGTTAGCCGGTTCCGCGCGTCGTCAGCCGGATGAAGTGCTCGATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGCTACGGCGGCGGTCGCTGGGACAAGCCGGCGCGGGACGGATGGCGCTGACGATATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGTGGCGTCCTGCGGGGGCCAGCCCGGAACTGCTACGTAAAGACGGCGAGCGTT 998
TCCCGCATCAGGCCGCGACCCAGGTTATTGCTGAACTGGAACCGTTCGACCGCGAACTGT
                                    TCCCACGTGAAGCGGCCCTGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGT
                                                                           CGCAAGAAAACGCACTGACTCTGGCCTGTCTGCCTGCATCCGACCCCCGCGCTGAGCGGTT 1298
                                                                                                                                                                                                                                     AGGCGATGAAAGAGGTACTGCGCGAACGCAGTAGTGAGTTACACGTTCCTTCTTCTCCAC 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ozenberger, B.A., Brickman, T.J. and McIntosh, M.A. Nucleotide sequence of Escherichia coli isochorismate synthetase gene entC and evolutionary relationship of isochorismate synthetase and other chorismate-utilizing enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli isochorismate synthase (entC)
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DSEGNGEWVVTIRCAKLRENQVRLFAGAGIVPASSPLGEWRETGVKLSTMLNVFGLH"
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MGDSPDSPFQOKLAALFADAKAQGIKNEVMVGAIPFDPRQPSSLYIPESMQSFSKQEK

QASARRFTRSQSLNVVERQAIPEQTTPEQMVARAAALTATPQVDKVVLSRLIDITTDSA

AIDSGVLLERLIAQNPVSYNFHVPLADGGVLLGASPELLLRKDGERFSSIPLAGSARR
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380. .1555
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/protein_id="AAA16100.1"
/db_xref="GI:450376"
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/EC_number="5.4.99.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Escherichia coli"
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AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K-12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 (e-mail: markeamber.gatech.edu). Open reading frames that have been correlated with genetic loci are being annotated with CG Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics. University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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                   /product="2,3-dlhydroxybenzoate-AMP ligase"
/protein_id="AAC73695.1"
/protein_id="AAC73695.1"
/db_xref="G1:1786810"
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GEROLSYRELNQAADNLACSULROGIKPGETALVQLGNVAELYITFFALLKLGVAPVL
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HNLQDAINHPAEDFTATPSPADEVAYFQLSGTTGTFKLIPTHNDYYYSVRRSVEIC
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/sub_strain="MG1655"
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/EC_number="6.3.2.-"
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/EC_number="5.4.99.6"
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Enterochelin"
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Dound_moiety="Ada predicted site"
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ALVPPAVSLMUQALLEGESRAQLASIKULQVGGARLSATHAARI PABIGCQLQQVFGM
AEGLVNYTRLDDSAEKI IHTQGY PMCPDDEWWADAEGNPLPQGEVGRLMTRGPYTFR
GYYKSPQHNASAFDANGFYCSGDLISIDPEGYITVQGREKDQINRGGEKIAEELENLL
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PEQQKVVDRLTPDADDTVLVKWRYSAFHRSPLEQMLKESGRNQLIITGVYAHIGCMTT ATDAFMRDIKPFMVADALADFSRDEHLMSLKYVAGRSGRVVMTEELLPAPIPASKAAL REVILPLLDESDEPFDDDNLIDYGLDSVRMMALAARWRKVHGDIDFVMLAKNPTIDAW .4630

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Biosynthesis of cofactors, carriers: P15047"

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/transl_table=11 /function="orf;
/note="o137; 10 100 Unknown"

O pct identical to YBDB_ECOLI . ws P15050"

/product="orf, hypothetical protein"
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/note="central position to predicted
/bound_moiety="MetJ predicted site" promoter:

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KEYWORDS
SOURCE
ORGANISM
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ECU82598
LOCUS
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AUTHORS
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                                                                                                                  Chung, E., Allen, E., Araujo, R., Aparicio, A., Davis, K., Duncan, M., Federspiel, N., Hyman, R., Kalman, S., Komp, C., Kurdi, O., Lew, H., Lin, D., Namath, A., Oefner, P., Roberts, D., Schramm, S. and Davis, R. Sequence of minutes 4-25 of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                  Escherichia coli genomic U82598
2 (bases 1 to 136742)

Roberts,D., Allen,E., Araujo,R., Aparicio,A., Chung,E., Davis,K., Duncan,M., Federspiel,N., Hyman,R., Kalman,S., Komp,C., Kurdi,O., Lew,H., Lin,D., Namath,A., Oefner,P., Schramm,S. and Davis,R.W. Direct Submission
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Bacteria; Proteobacteria;
                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYFRONGYHSDOMNNIGTWYORALIILKSEL/MGDONTGSDIFDGVGFRGVRLYSDN
MYFDSQOGFAPTVRGIARTAQUTIIRQNGFIIYGSYVSPGAFFITDLHPTSSNGDLDV
TIDERDGNQORNTIFYSGTVPILOREGRRYEDLITAGDFRSGNSQOSSPFFGGGTALGGL
POETTAYGGTQLSANYTAFLLGLGRULGNWGAVSLDYTHARSQLADASRHEGDSIRFI
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RAKSMITFGTNFQLMGYRYSTYGFFYTLDDVAYRAWSTYDYGYTSSWYGISYSLS
SWNESYGIPDMERIVGLNVSVPTNGTRRYTRENALDRAVASFTNANGNSNGLNSWLA
GYGGTLLEGHNLSYHVSQSLNDFGSLYIGTHAKYNTRENALDRAVASGTLAGGYNYTDDQHDVNWQL
SGGVVGHENGTTLSQPLGDTNVLIKAPGAGGYNIENOTGILTDWRGYAWTLATVYRY
SGRVVGHENGTTLSQPLGDTNVLIKAPGAGGYNIENOTGILTDWRGYAWTLATVYRY
RIALDTNTNNNSIDDEKNISYVPTGGALVBANEDTRIGVRALTYTTGGGRVPFFGS
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3835...
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KSIAVKCTNVAAQAYLTMRLEASAVSGQAMVSDNQDLGFIVADQNDTPITPNDLNSVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mkiptttdipqrytwclagicysslailpsflsyaesyfnpafl
/engtsyadlsreeronhopagyrydlwrindffigsquiyfsgttentgoksgglwp
Cfnqylleriglnssafpelaqoqnincinlkaypdatinfdpdaamrlitipqia
LSSAHGYIPPEEWDEGIPALLLNYNFTGNRGNGNDSYFFSELSGINIGPWRLRNNGSW
                                                                                                                                          as C. briggsae
3835. .4476
                                                                                                                                                                                                                      complement(3267.
                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB40731.1"
/db_xref="GI:1778448"
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/codon_start=1
/transl_table=11
/product="FimH homolog"
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                                                           /note="similar
                                                                            /gene="ybcG"
                                                                                                                                                                              /note="previously sequenced by another found in GenBank Accession Number R038
                                                                                                                                                                                                                                                                                                         PPQNYIRMGTDPNVSQNLPFGVMDSRLIFRLKVIRPFINMVEIPRQVMFTVYVTSTPY
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/db_xref="GI:1778447"
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/db_xref="taxon:562"
/map="minutes 9 to 12"
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                                                                                                                                                                                                                                                /translation="MTFSFLCYAITRAHLDSMQRRLKRRNAGLPCCEVPGYYREDASS PLLPKKKTNESQCLVHRFDELRHHLVKTRHVLFIPLNHDIMQAFTLHARVIVGKVPGI FSREDHAVHLGHVSRFYLETTEPEFHEIPGTSIAGSVACIRMQSLIRGNRTRITG WLPTCTRTCGPMRWLTRNYGARLPMN"

join(6717. .7407,8666. .9383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSLFRRNEIWYASYSLPGGKRIKESLGTKDKRQAGELHDKRKAE LWRUEKLGDLPDVTFEEACLRRLEEKADKKSLDSDKSRIEFWLEHFEGIRLKDISEAK IYSAVSRMHNRKTKEIWKQKCLRRLEEKADKKSLDSDKSRIEFWLEHFEGIRLKAHIKALIRAA ERDWKWLEKELWYVEFAFVYSTQTKAKHLAMIKALIRAA ERDWKWLEKAPVIKIPAVRNKRVRWLEKEEAKRLIDECPEDLKSVVKRALATGLRKSN INLEWQQIDMQRRVAWVNPEESKSNRAIGVALNDTACKVLRDQIGKHHKWVFYHTKA AKRADGTSTPAVRKMRIDSKTSWLSACRRAGIEDFRFHDLRITWASWLIQSGVPLSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="previously sequenced by another group and can found in GenBank Accession Number X51662" complement(4479. .5174)
/gene="fim2"
                                                                                                                                                                                                                                                                                                                                                                                                                                             QEMGGWESIEMVRRYAHLAPNHLTEHARKIDDIFGDNVPNMSHSEIMEDIKKA" 6603. .7163
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GKNSELQIVLKTDDYRITIDYLRTRPVDLIIMDIDLPGTDGFFFLKRIKQIQSTYKVL
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CSTNSSTVTVLSNREVTILRYLVSGLSNKEIADKLLLSNKTVSAHKSNIYGKLGLHSI
VELIDYAKLYELI"
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/note="prophage DLP12 integrase"
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                                    /organism="Escherichia
                                                                                                                                               /transl_table=11
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/db_xref="GI:1778449"
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563 ATGATGAATTGTTTATTTCAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGA 622
GTTCCATGTATGTGAATCAAACGCAGCGACGAGCAACTTTATTTGCTGGTGCCGGGATTG
                                                                                                                                                                                                         TCCCACGTGAAGCGGCCCTGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGT
                                                                                                                                                                                                                                                                           CGCAAGAAAACGCACTGACTCTGGCCTGTCTGCTGCATCCGACCCCCGCGCTGAGCGGTT
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                                                                         TTGGCGGCATTGTGGGTTGGTGACAGCGAAGGTAACGGCGAATGGGTGGTGACCATC
                                                                                                                       TTGCAGGTCCTATTGGCTATTTTACCGCAGATAATAGTGGGGAATTTGTGGTTGGCATCC
                                                                                                                                                                          TCCCGCATCAGGCCGCGACCCCAGGTTATTGCTGAACTGGAACCGTTCGACCGCGAACTGT
                                                                                                                                                                                                                                                                                                                                                                         AGCTGATCACCACGCCGACGCTGTGGCATCTCGCAACTCCCTTTGAAGGTAAAGCGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCGATGAAAGAGGTACTGCGCGAACGCAGTAGTGAGTTACACGTTCCTTCTTCTCCA
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8461. .9705
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SPVSYSAHGLFVSENLLEODFYASGPNOKWAGDITYLETDEGHYLAVVIDLWSRAVI
GWSMSPRMTAOLACDALOMALWARKRERNVITUTDRGGOYCSADYQAOLKERHULRGSW
SAKGCCYDNACVESFFHSLKVECIHGEHFISREIMRATVFNYIECDYNRWRRHSWÇGG
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/protein_id="AAB40739.1"
/db_xref="GI:1778456"
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/protein_id="AAB40738.1"
/db_xref="GI:1778455"
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/codon_start=1
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/db_xref="GI:1778454"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="previously sequenced
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/ESQLYNWRSKQQNQQTSSERELEMSTEIARLKRQLAERDEELAILQKAATYFAKRLK
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Pred. No. 4.8e-12
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Heidelberg, J.F., Elsen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, M.L., Heidelberg, J.F., Elsen, J.A., Heckey, E.K., Peterson, J.D., Umayam, L.A., Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A., Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.D., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JUN-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:666"
/chromosome="1"
/note="biotype: El To:
128. 718
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                                                                                                                                                                                                                                     /translation="marrndhtreelvaltldrvkgfldthsyhelslrkvatmigyv
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yhgitilsyddkffanefidgnalinnllnhylanw"
                                                                                                                      /gene="VC1966"
722. .2602
                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
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/db_xref="GI:9656505"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="VC1965"
/note="identified by Glimmer2; putative"
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128. .
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                                    /gene="VC1966"
/note="identified by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'VC1965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 El Tor"
                                        Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80999
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/note="similar to GB:U00096 SP:P77626 PID:1742340 PID:1742346 PID:1787704; identified by sequence similarity: putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VC1967"
2778. .4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Translation="MNKMANPTTALLTERRFLPYFITOFLGA!*NDNIFKNVLLLEVAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTSEATTHQEQSVTSIASSLSHLOALCQSAQEKIQQSEHTISALKLKQEDLALKMSKFKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to PID:1255679; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \verb|ANNRASLRRAFADIEHSLNEGNLVCIFPEGRLTADGEMNPFMRGLDLILHRSPVPVVPLALKGLWGSYFSRYKGRACQGVPRRFRSQLEIEAGMPVAPEQANSAVMHEKVAQLRGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5442. .5537)
/gene="VC1969"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4885. .5430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKLETLGDSAVEELEREPNRNITWQSDVMERWQAADGGMESNIGLLWKLYYTQRLLDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (5442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYAAVTEKAVFQNIVAYPRRG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4885. .5430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNTIQQSITQLRSSADESVRVINNSMLKGTQTTEITSQAEESLHQVAIEISRLTQMNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="methyl-accepting chemotaxis
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/db_xref="GI:9656507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVCLSVLEMSIPQLFALLAVLNVLVALYIFLQVPIFAVRFLVWILTHTLYRVRHKNLH
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                                                                                                     /gene="VC1970"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="VC1969"
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                                                                                                                                           .6681
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Query Match
Best Local Similarity
Matches 282; Conserv
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574 TTTATTTCAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCG 633
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="o-succinylbenzoate-CoA synthase"
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/gene="VC1973"
complement(9202..10092)
/gene="VC1973"
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NEDVDQDKAQRYRAVLWAGGFYLLAGIFAALVVNLFLALPKPISAMLAGLALLGTLMM
CLQSAFKIDEYREPALLTFVITLSGATLFGMSATLIGLVIGLAYLRLTTRPRP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="g1:9656510"
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                                                                                                                                                                                                                                                                                                                                                                                               EELERETVRWCREVLQHSPMAIRCLKAALNADCDGQAGLQELAGNATMLFYMTEEGQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:M93421
PID:1788597; identified by s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:L07256 SP:P29208 PID:146811 GB:U00096
PID:1788596; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8116. .9114)
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PID:1788595; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(6710. .8140)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDGGIKVSRAAVKAWLAANQTQFTPL"
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                                                                                                                                           46.5%;
                                                                                             0;
                                                                                             Score 74; DB 1; Lo
Pred. No. 1.5e-11;
0; Mismatches 315;
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sequence similarity; putative"
                                                                                                                                                                                          Length 14027;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCGAC 12610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTGCTGAGCATGAATGGCAGGAGCTGGATAAAAAGCTCTCTACCTTATTGAGCTTGATA 12616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCGCAACAAGAATATGAAGAAACTGGGTTGAAATTTGAACCCATGCGGCAATTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGGTTACTTTAGCCATGCGCAAGCCGAGTTTTGTGTGGCGATCCGCAGTGCTTTAGTG 12727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTGGCTATTTTACCGCAGATAATAGTGGGGAATTTGTGGTTGGCATCCGTTCCATGTAT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGCCCTGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGTTTGCAGGTCCT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGACCGCGATTGTTGACCGCTTGCATCCAACACCAGCACTGGGTGGCGTCCCACGTGAA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAAGCAAGTTCAGCATTTGTACACACCAATTACAGGGGACATTGCGGCACATTTAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACACGCTTGCAAGACGTGACGACGTCGCTAAAAGGTGCCGGCCATGCCAAGTTTACTCAAA 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCTGACGCATGACAGTAAAAACCTCAATGAAAATCAGTTGGTGGTAGAGGACATCATC 13027
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                                                                                                                                                                                                                                                                                                                                   E.coli DNA, clone pME2541.
Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                   ECOENTCE 1302 bp DNA
E. coli iron chelator protein
chelator protein (entE) gene,
                                                                                                                                                                                                                                                                     1 (bases 1 to 1302)
Elkins, M.F. and Earhart, C.F.
                                                                                                                                                                                                                                                                                                                                                                                                   M36700.1 GI:145839
                                                                                                                                                                                                                                                                                                                                                                                                                    M36700 X12670
                                                                                                                                                                                                   90236256
                                                                                                                                                                                                                  homology to trpE and pabB
FEMS Microbiol. Lett. 56,
                                                                                                                                                                                                                                                      An Escherichia coli enterobactin
                                                                                                                                                                                                                                                                                                             Escherichia.
                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                       94. .1269
                                                                                                       /db_xref="taxon:562"
45. .64
                /gene="entC"
                                                                                                                                           /organism="Escherichia
                                                                                                                                                                             Location/Qualifiers
/codon_start=1
                                                /gene="entC"
                                                                                      bound_moiety="Fur"
                                                                                                                                                                .1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ACAAGTTCAGCTCTATGCAGGCGCTGGCATTGTGCCGGGCTCG 12676
                                                                                                                                                                                                                    35-40
                                                                                                                                                                                                                                                                                                                                                                                 chelator protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     (entC) gene,
5' end.
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                                                                                                                                                                                                                                                        gene
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803
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                                                                                                                                                                                           GTTCCATGTATGTGAATCAAACGCAGCGACGAGCAACTTTATTTGCTGGTGCCGGGATTG
                                                                                                                                                                                                                                                                          TTGCAGGTCCTATTGGCTATTTTACCGCAGATAATAGTGGGGAATTTTGTGGTTGGCATCC
                                                                                                                                                                                                                                                                                                                                                                         TCCCACGTGAAGCGGCCCTGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCAAGAAAACGCACTGACTCTGGCCTGTCTGCTGCATCCGACCCCCGCGCGTGACGGCTT
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GGCAATTGTT 1172
                                                                                                                                             GCTGCGCGAAGCTGCGGGAAAATCAGGTGCG-----TCTGTTTGCCGGAGCGGGATTG
                                                                                                                                                                                                                                                                                                                                          TCCCGCATCAGGCCGCGACCCAGGTTATTGCTGAACTGGAACCGTTCGACCGCGAACTGT
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                                              TGCCTGCGTCGTCACCGTTGGGTGAGTGGCGCGAAACAGGCGTCAAACTTTCTACCATGT
                                                                                            TGGCTGACTCCGATGCGCAACAAGAATATGAAGAAACTGGGTTGAAATTTGAACCCATGC
                                                                                                                                                                                                                                              TTGGCGGCATTGTGGGTTGGTGACAGCGAAGGTAACGGCGAATGGGTGGTGACCATCC
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LATPFEGKANSQENALTLACLLHPTPALTAFPHQAATQVIAELEPFDRELFGGIVGWC
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NGDSPDSPFQQKLAALFADAKAQGIKNPVMVGAIPFDPRQPSSLYIPESWQSFSRQEK
QASARRFTRSQSLNVVERQAIPEQTTFEQMVARAAALTATPQVDKVVLSRLIDITTDA
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/product="iron chelator protein"
/protein_id="AAA18491.1"
/db_xref="GI:145840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSEGNGEWVVTIRCAKLRENQVRLFAGAGIVPASSPLGEWRETGVKLSTMLNVFGLH"
1279. .1302
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/product="iron chelator protein"
/protein_id="AAA18492.1"
/db_xref="GI:145841"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="entE"
/codon_start=1
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1279. .>1302
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46.28;
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Pred. No. 2.7e-11;
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Escherichia coli menaquinone specific isochorismate synthase (gene, complete cds and SHCHC synthase/KDC (menD) gene, partial U54790 U54790.1 GI:1399683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daruwala,R., Kwon,O., Hudspeth,M.E.S. and Meganathan, Menaquinone (vitamin k-2) biosynthesis: evidence for (menF) encoding an alternate isochorismate synthase ASM Abstracts 94, 303-303 (1994)

2 (bases 1 to 1560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-APR-1996) Michael E. S. Hudspeth, Biological Sciences, North Illinois University, Dekalb, IL 60115-2861, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hudspeth, M.E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Daruwala, R., Kwon, O., Meganathan, R. and Hudspeth, M. A new isochorismate synthase specifically involved (vitamin K2) biosynthesis encoded by the menf gene FEMS Microbiol. Lett. 140 (2-3), 159-163 (1996)
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1475. .
                                                                                                                                                                                                                                                                                                                                                                          /product-"isochorismate synthase"
/protein_id="AAC44303.1"
/protein_id="AAC44303.1"
/db_xref="G1:1399684"
/translation="MOSLITALENLLRHLSQEIPATPGIRVIDIPFPLKDAFDALSWL
/translation="MOSLITALENLLRHLSQEIPATPGIRVIDIPFPLKDAFDALSWL
ASQQTYPQFYWQQRNCDEEAVVLGATRFTSLDQAQRFLRQHEPHADLRIWGLNAFDP
SQGNLLLPRLEWRRCGGKATLRLTLFSESSLODAIQAKFIATTLYSIKPLFQCHLTT
TREOHWPDKTGWTQLIELATKTIAEGELDKYVLARATDLHFASPYNAAAMMAASRRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MenF"
/note="menaquinone specific;
encoded by Genbank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MenF"
94. .1386
                                                           /product="SHCHC synthase/KDC"
/protein_id="AAC44304.1"
/db_xref="GI:1399685"
                                                                                                                                                                                                                                                                                                                 LNCYHFYMAFDGENAFLGSSPERLWRRRDKALRTEALAGTVANNPDDKQAQQLGEWLM
ADDKNQRENMLVVEDICQRLQADTQTLDVLPPQYCLRKVQHLRRCIWTSLNKADDVIC
LHQLQPTAAVAGLPRDLARQFIARHEPFTREWYAGSAGYLSLQQSEFCVSLRSAKISG
                     /translation="MSVSAFNRRWAAVILEALTRHGVRHICIA"
407 c 407 g 368 t
                                                                                                                                                                      decarboxylase"
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/transl_table=11
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                                                                                                                                                                                                                                                      Arabidopsis thaliana AF078080
                                    Meng, H., Peter, G. and Pullman, G.
Direct Submission
Submitted (14-JUL-1998) Forest Biology, and Technology, 500 10th St. Atlanta, G.
                                                                                                                              Meng,H., Pullman,G.Ś. and Peter,G.F. Cloning of a Plant Isochorismata sum
                                                                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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Tegelen, L.J.,
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574 TTTATTTCAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCG 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTATAAAATATTGGCTGCTGCATCCAACTCCAGCTGTTTGTGGGCTTCCAGCAGAA 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGACCGCGATTGTTGACCGCTTGCATCCAACACCAGCACTGGGTGGCGTCCCACGTGAA 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAAGCAAGTTCAGCATTTGTACACACACCAATTACAGGGGACATTGCGGGCACATTTAAGT 873
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                                                                     isochorismate synthase.
Madagascar periwinkle.
Catharanthus roseus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae;
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AJ006065.1 GI:4127687
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                                                     Catharanthus
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                             (bases 1 to 2078)
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SAVFFRDLDPFSCHDDWRS IRRFLSSTPPLIRAYGGMREDPGKIAVEWEFGAFFFSV
PQVEFNBEGGSSMLAATLAWDDELSWTLENA IEALQETMLQVSSVVHKLRNRSLGVSV
LSKNHYPTKGAV FPAVEKALEMINQKSSPLNKVVLARNSRIITDTDIDPIAWLAQLOR
EGHDAYOFCLQPPGAPAFIGNTPERLFRORTFLLGVCSEALAATRAFRAASSARDWBIERD
LLTSFRDDLESSIVFBNI REKLNXICDRVVKPQKTVRKLARVGHLYSQLARRLTKBD
DEYKILAALHPTPAVCGLPAEEARLLIKEIESFDRGMYAGPIGFFGGEESEFAVGIRS
ALVEKGLGAALITAGTGIVAGSDPSSENNELDLKISGTTKSIEYEATTSLQAIN*
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45.8%;
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  Moreno, P.R.,
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Pred. No. 3.3e-07;
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  Croes, A.F.,
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Best Local S
Matches 172
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1679 AAGGAAGTGATCCAGCTCTAGAATGGCAGGAACTAGAGCTCAA
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mes 172; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   van Tegelen,L.

Direct Submission
Submitted (OB-MAY-1998) van Tegelen L., Department of Experimental Botany, University of Nijmegen, Toernooiveld 1, 6525 ED Nijmegen, THE NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purification and cDNA cloning of isochorismate synthase from elicited cell cultures of Catharanthus roseus Plant Physiol. 119 (2), 705-712 (1999)
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nilarity 50.1%;
Conservative
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GLYAGPWGFFGGAQSDFSVGIRSALIGKDAGALIYAGLGVVEGSDPALEWQELELKAS
QFMKLKKLEAPALK"
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/strain="G. Don (Madagascar periwinkle)"
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Result
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                         Streptococcus pneu
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S. pneumoniae deri
Staphylococcus aur
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Staphylococcus aur
Enterococcus faeca
E. coli entC DNA.
C. roseus ICS DNA.
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                Enterococcus faeca
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Q12159	27	Z46355	V52162	T77805	T77 806	T77803	X75759	X13086	Z46368	T67241	T77804	X60243	Z37314	A05526	T97221	X1 3316	X13159	V66834	Z30446	Q89692	N80872	X20535	X12960	X07180	Z12105	Z12106	Z23937	X30483	T68178	СŃ	044	X88786	
	Streptococcus pneu	The second		encoding	cDNA encoding vari	cDNA encoding wild	1	Enterococcus faeca	Haemorrhagic enter	Pasteurella haemol	cDNA encoding vari	Domain IV sequence	Human ion transpor	Streptococcus pneu	Ð		Enterococcus faeca	Zea mays soluble s	Tobacco anthranila	pepR. Lactococcus	Nucleotide sequenc	Polynucleotide seq	Enterococcus faeca	Corn threonine dea	Neisseria meningit	μ.		pylori	H. pylori cell env	Streptococcus pneu	Tobacco anthranila	Cyclotella cryptic	

ALIGNMENTS

RESULT 1 V41196

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Human; neutral sphingomyelinase; N-SMase; diagnosis; Crohn's disease; obesity; diabetes; Alzheimer's disease; ss.
        Chatterjee S;
                            (UYJO ) UNIV JOHNS HOPKINS
                                                 24-DEC-1996;
                                                                    23-DEC-1997;
                                                                                         02-JUL-1998.
                                                                                                             WO9828445-A1
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                    Human neutral sphingomyelinase encoding cDNA.
                                                                                                                                                                                                                                                                                        20-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                               V41196;
                                                                                                                                                                                                                                                                                                                                  V41196 standard; cDNA; 1197
                                                 96US-0774104
                                                                     97WO-US24051
                                                                                                                                /product= "neutral sphingomyelinase"
/transl_except= (pos:175..180,aa: %al residues but only onc ,
/note= "appears to encode 2 Val residues but only onc ,
is given in the amino acid sequence (%69162)"
                                                                                                                                                                                     Location/Qualifiers
1..1197
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                                                                                                                                                                                                                                                                                                                                  BP
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The present sequence encodes human neutral sphingomyelinase (N-SMase).

CC A host cell containing a vector comprising a nucleotide sequence concoding N-SMase can be used to produce N-SMase. N-SMase can be used in a method for identifying a compound useful in the diagnosis or treatment concleotide sequence encoding N-SMase related disorder. N-SMase, and a concleotide sequence encoding N-SMase, can be used for modulating N-SMase can be used for modulating N-SMase can be used for modulating N-SMase. The concleotide sequence or conservation, inflammatory disorder, arthritis, osteoarthritis, crohn's conservation, inflammatory disorder, arthritis, osteoarthritis, contral conclusion system disorder, vascular restenosis, arterial occlusion arising conservation, cardiac disease where LV dysfunction occurs, chypercholesterolaemia, cholesteryl ester storage disorder, renal failure, contral infection, depression, schizophrenia, neurodegeneration, and contral conclusion and contral conclusions and contral co
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Best Local Similarity
Matches 1197; Conser
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                                                                                                                                       TTATCCGACACGTTACGACTGGCACAAATTATTCGTGCGTTAGCTGAGCAGGCGAATACG
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the sequence listing in the specification are included to maintain the nucleotide num
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents one of 5191 Staphylococcus aureus DNA sequences CC of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using Ct the S.aureus DNA sequences allows putative functions to be assigned so CC that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are CC likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC saureus in a sample. S.aureus is implicated in numerous human diseases, CC including cellulitis, eyelld infections, food poisoning, osteomyelitis, CC skin and surgical wound infections, scalded skin syndrome, toxic shock CC syndrome, etc. Organisms transformed with the DNA sequences can be used CC (and their fragments) are useful as primers or probes for isolating CC homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 354
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                                                                                                                                     GAAGCGTTGGTTAGCCAGTCAGAAAAAACCGCATTGAACATCAATATGTCGTGGCAAGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                            GTCGTTTTTGGTCGGCAACAGACCCTGCAGTTATCCGACACGTTACGACTGGCACAAATT
AAAAATAAGCAAGTTCAGCATTTGTACACACCAATTACAGGGGACATTGCGGGCACATTTA
                                                                                                                                                                                      AAAGCTGTAGCAGGTACAATTAAACGTTCACAAGATGAGGACGAAGATACAAAAAATGTT
                                                                                                                                                                                                                       GCGGCGGTCGCTGGGACAAGCCGGCGCGCGGGACGGATGGCGCTGACGATATCGCGTTAGGC
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                                                                                                                     GAAGCATTTTTAAAAAGATAATAAAAACTTAATCGAACATCGATTTGTTGTTGACAGTATT
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                                                                                                                                                                                                                                                                                                                           NNGCAAGCATATTCTAAAGAAAAAAAAACAGTTATATATTCTTGTTAGAATCACAAGATTCT
                                                                                    ACGACACGCTTGCAAGACGTGACGACGTCGCTAAAGGTGCCGGCCATGCCAAGTTTACTC
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Pred. No. 4.7e-33;
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used
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                                                                                                        Claim 1;
                                                                                                                                           use in vaccines
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                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                               16-MAY-1997;
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06-MAY-1997;
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                                                                                                                                        isolated Enterococcus faecalis polynucleotides and polypeptides sed to develop products for the detection of Enterococcus and for in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                        1999-045171/04
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                                                                                                       Page 438-444;
                                                                                                                                                                                                               Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                          faecalis
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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer based system can identify fragments of the Enterococcus faecalis genome with

can identify fragments of the Enterococcus faecalis genome wit commercial importance. The products can be used to detect the of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring

be used for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                    1017
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                                                                                                                                                           AACTGGGTTGAAATTTGAACCCATG 1161
                                                                                                                                                                                                           cgttctttatgcaggttgtggtattgttgcggattcccaagcagagctagaaagagaaga
                                                                                                                                                                                                                               AACTTTATTTGCTGGTGCCGGGATTGTGGCTGACTCCGATGCGCAACAAGAATATGAAGA 1136
                                                                                                                                                                                                                                                                                 tagtggcgagttcgctgtggccttgcgttcaggtgtctttgctggtcagca----agg
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                                                                                                                                           Query Match
Best Local Similarity 46.b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linthorst HJM, Verpoorte
Van Tegelen LJP, Wullems
Simons LH, Melchers LS,
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entC; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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03-APR-1998;
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(UYLE-) RIJKSUNIV LEIDEN
(UYNI-) UNIV NIJMEGEN.
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DB; Y50335, Y33698
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CGTTAGGCGAAGCGTTGTTAGCCAGTCAGAAAAACCGCATTGAACATCAATATGTCGTGG
                             ttagctccattccgttagccggttccgcgcgtcgtcagccggatgaagtgctcgatcgcg 1058
                                                            Page 51-53; 66pp; English.
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98US-0080625
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Croes AF,
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                                         (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
(UYNI-) UNIV NIJMEGEN.
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  Van Tegelen LJP,
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               Linthorst HJM,
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P, Wullems (
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Verberne MC, Moreno PR
Croes AF, Stuiver MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                       ccus pneumoniae;
readable medium;
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Pred. No. 1.2e-08;
0; Mismatches 16!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 G;
                                                                                    fragment
                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642 T; 0 other;
                                                                                     SEQ
                                                        genome;
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                                      diagnosis; as:
l composition;
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1;

Streptococcus

pneumoniae

WO9818931-A2

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The present invention describes a computer readable medium which has C the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded CC on it, or a representative fragment or a sequence at least 95% identical CC SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus CC pneumoniae. The present invention also describes an isolated nucleic acid CC molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced CC by a process comprising: (a) screening a genomic DNA library using as a CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences (and the sequences of the target sequence and isolating the nucleic acid completer to the target sequence and isolating the nucleic acid completer to the target sequence and isolating the nucleic acid completer sequence is homologous to amplification primers derived from the sequences of the S. pneumoniae genome to prime the amplification and collating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present CC invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10357 BP; 2979 A; 2388 C; 1821 G; 3169 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1151-1157; 1409pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 AAGTTCAGCATTTGTACACCCAATTACAGGGGACATTGCGGCACATTTAAGTGTGACCG
AACAAGAATATGAAGAAACTGGGTTGAAATTTGAACCCATG 1161
                                                               TCAAAAATCAAAGAGCCTATGTGCAGGCTGGGGCAGGGATTGTCTACGACTCTATCGCCC
                                                                                                AAACGCAGCGAGCAACTTTATTTGCTGGTGCCGGGATTGTGGCTGACTCCGATGCGC
                                                                                                                                                                                                                                   TGAGACGTATCTATGAACTGGAAACGGAAAAACGGGGAGTATACGCTGGGGCAATCGGCT
                                                                                                                                                                                                                                                                                                                                                                                         TGTATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGTTTGCAGGTCCTATTGGCT
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Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 0.0027;
0; Mismatches 173;
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Sequence 5057 BP; 1171 A; 1554 C; 1302 G; 1030 T; 0 other;

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                                                 harboring a gene coding for an isochorismate synthase (ICS), A pathogen inducible promoter can be used to drive expression of a hetcrologous protein. The heterologous protein used in the method of the invention is an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins, saccharide oxidase, oxalate oxidase, magainins, toxins from Bacillus thuringiensis, or antifungal proteins isolated from Mirabilis jalapa, Amaranthus, Raphanus, Brassica, Sinapis, Arabidopsis, Dahila, Cnicus, Lathyrus, Clitoria, Allium seeds, Aralia and Impatiens and albumin-type proteins, such as thionine, napin, barley trypsin inhibitor, cereal gliadin and wheat-talpha-amylase, or a protein that can induce a hypersensitive response, such as Cf, Bs3 and Po proteins from tomato and Protein from tobacco. This sequence encodes the Pseudomonas fluorescens
                          isochorismate synthase orfA protein and the isochorismate pyruvate lyase orfD protein which are described in the method of the invention.
                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                            Method for inducing pathogen resistance
                                                                                                                                                                                                                                                                                                                                         WPI; 1999-610856/52.
P-PSDB; Y50336, Y50337, Y500338, Y50339
                                                                                                                                                                                                                                                                                                                                                                                                                     Linthorst HJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5858 AAAACGAATACCAAGAAAACCATTAACAAAGCAAAATCTATG
                                                                                                                                                                                                                                       This invention describes a novel method for the induction of pathogen resistance in plants, by transformation with an expression cassette
                                                                                                                                                                                                                                                                                                                                                                                         Simons LH,
                                                                                                                                                                                                                                                                                                                                                                                                       Van Tegelen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1999;
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, Wullems
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98US-0080625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "isochorismate pyruvate lyase orfD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! NV.
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Croes AF,
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  Complete genome sequence
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                                                                                                                                                                                                                                 Methanococcus
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                                                                                                                                                                                                                                                                                              Methanococcus jannaschii circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                     caagccccgactccgaatgggcagaagtccagaccaaacttggcaccatcgtgc
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                                                    Smith
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                                                                                                                                                                                                                                                          extrachromosomal element; identification;
                                                   Venter
of methano-genic archaeon, Methanoccoccus
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                                                   JC,
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                                                   White OR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the Methanococcus jannaschil circular chromosome. The present invention describes M. Jannaschil circular chromosome. The genome sequence. The invention also describes a computer based system for identifying fragments of the M. Jannaschil genome that are homologous to target nucleotide sequences, comprising: (a) data storage means comprising the nucleotide sequence of the 164976, 58407 or 16550 by sequence (see v21209, v21210 and v21211), or a nucleotide sequence at least 99.9% identical to it; (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means to identify a homologous sequence, and (c) retrieval means for obtaining the homologous sequence. The method, which is based on whole genome of which consists of 3 physically distinct elements, a large circular extra-chromosoma (the 164976 by sequence given in v21209), alarge circular extra-chromosomal element (the 58407 bp sequence given in v21210), and a small circular extra-chromosomal element (the 16550 bp sequence given in v21210), and a
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Best Local
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fragment
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caatcccagaaaatgaatgggaagagacagagagaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTGCAAGACGTGACGACGT-----CGCTAAAGGTGCCGGCCATGCCAAGTTTACTCA 811
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                                                                                                                                     ATGTGAATCAAACGCAGCGACGAGCAACTTTATTTGCTGGTGCCGGGATTGTGGCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 152-585;

    useful in

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used in the identification of M. jannaschii genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.08;
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                                                                                       -ggatatattcaagttggtgctggaattgtagctgatt
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    458118
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel isolated Streptococcus pneumoniae polynucleotides (see 296173-296494) and their encoded proteins (see 185792-186182). The DNA, vectors and host cells described in the method of the invention are useful for the recombinant expression of the polypeptides. The polypeptides are useful for treatment or prevention of disease, or diagnosis of disease related to expression or activity of such a polypeptide. They can also be used to screen for compounds which interact with and inhibit or activate such a polypeptide. The polypeptides (or DNA encoding them, via gene therapy) are also useful for inducing an immunological response in a mammal. The antagonists are useful to inhibit such bacterial polypeptides. The polypeptides are particularly useful to identify antimicrobial compounds and antibiotics. They are also useful to determine their role in pathogenesis of infection, dysfunction and disease.
                                                                                                                                                                                                                                1149
                                                                                                                                                                                                                                                       1055 TGAATCAAACGCAGCGACGAGCAACTTTATTTGCTGGTGCCGGGATTGTGGCTGACTCCG 1114
             Staphylococcus aureus contig
                                        16-MAR-1999 (first entry)
                                                                                                 V74332 standard; DNA; 3647
                                                                                                                                                                        1089 TCGCCCAAAACGAATACCAAGAAAC
                                                                                                                                                                                                  1115 ATGCGCAACAAGAATATGAAGAAAC 1139
                                                                                                                                                                                                                                                                                                                                                            Sequence 1167 BP; 319 A; 280 C; 228 G; 340 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae proteins and screening compounds for antibacterial
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bacterial;
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                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                           TGATTCTCAAAAATCAAAGAGCCTATGTGCAGGCTGGGGCAGGGATTGTCTACGACTCTA 1090
                                                                                                                                                                                                                                                                                       1 Similarity
53; Conserv
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antimicrobial; antibi
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                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                 2.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sease; diagnosis;
antibiotic; path
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                                                                                                 ВÞ
                                                                                                                                                                                                                                                                                     0;
             SEQ ID #21.
                                                                                                                                                                                                                                                                                                 Score 33.8; D
Pred. No. 0.5;
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                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osis; gene therapy; scree pathogenesis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lonetto MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related DNA - activity
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811 AAAAATAAGCAAGTTCAGCATTTGTACACACCAATTACAGGGGGACATTGCGGCACATTTA 870

anatatgaacatgttatgcatatcgtaagtgaagtcacaggtaaaatanaatcanaattta 622
AGTGTGACCGCGATTGTTGACCGCTTGCATCCAACACCAGCACTGGGTGGCGTCCCACGT 930

Matches

Similarity

2.7%;

Score 32.4; Pred. No. 2

1; DB 18; 2.8; ches 191;

Length Indels

-5;

Gaps

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Mismatches

Conservative

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for the composition of the composition of the composition of the composition and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for the composition of the composition of the composition of the DNA sequences can be used for the composition of the composition of the composition of the DNA sequences can be used for the composition of the DNA sequences can be used for the composition of the DNA sequences can be used for the composition of the DNA sequences can be used for the composition of the DNA sequences can be used for the composition of the DNA sequences can be used for the composition of the DNA sequences can be used to the the DNA sequences can be used to the DNA sequences can be used 
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Sequence 3647 BP; 1315 A; 550 C; 619 G; 1037 T; 126 other;
                                                                                             computer readable
                                                                                                                                    for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-S.aureus vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-374922/35
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                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                    can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the
                          another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                          982 nucleotide sequences isolated from the Enterococcus faecalis X12938 to X13919 represent these nucleotide sequences which are nucleotide sequences, also known as contigs. The computer-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1051
                                                                                                                                                                                                                                                                                                                                          WPI; 1999-045171/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 TCCGATGCGCAACAAGAATATGAAGAAACTGGGTTGAAATTTGAACCCATGCGGCAATTG
                                                                                                                                                                                                                                     Claim 1; Page
                                                                                                                                                                                                                                                                                             New isolated Enterococcus faecalls polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for
                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN
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                                                                                                                                                                                  computer readable medium has been developed which has recorded on it
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Best Local S
Matches 70
               recombinant phage DNA. The PEP4 prod., a vacuolar, aspartyl protease capable of self-activation, as well as subsequent activation of additional vacuolar proteases, e.g. carboxypeptidase and proteinase B may be mutated to create a proteolysis-deficient strain of Pichia which may be used for recombinant expression of proteolytically sensitive proteins, e.g. EGF, GRF and IGF-1. See also Q29938-41.
                                                                                                                                        a lambda based EMBL3 P. pastoris genomic DNA library by its ability to hybridise with a radiolabelled fragment of the homologous Saccharomyces cerevisiae PEP4 gene. The P. pastoris PEP4 gene was cloned by isolating positive plaques contg. the hybridising recombinant phage DNA. The PEP4 prod., a vacuolar accombinate pages of contents of cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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                                                                                                                                                                                                                                                                                                                                     Claim 7;
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                                                                                                                                                                                                                                                                                                                                                                                                         New isolated DNA fragment from Pichia comprising gene influencing proteolytic activity - used to generate proteolytic deficient strains, as hosts for expression of proteolytically sensitive
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SQ

Sequence

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Best Local :
                                                                                                        exon
Jarvis EE,
                             03-APR-1996;
                                                                                                                                                    exon
                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                      phosphoglucomutase;
carbohydrate; ds.
                                                                                                                                                                                                                                                                                                                     Cyclotella cryptica;
                                                                                                                                                                                                                                                                                                                                    Cyclotella
                                                                                                                                                                                                                                                                                                                                                                                X88786 standard;
              (MIDE ) MIDWEST RES INST
                                            03-APR-1996;
                                                           27-JUL-1999
                                                                          US5928932-A.
                                                                                                                              intron
                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                         Cyclotella
                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                    427 aaatgctttgtccaagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                    564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 AGCCAAAGTCGTTTTTGGTCGGCAACAGACCCTGCAGTTATCCGACACGTTACGACTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAAATTATTCGTGCGTTAGCTGAGCAGGCGAATACGTATCATGTGGTTTTTAAAGCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATGAATTGTTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  caattttgggcagtatgtctctgctctggaacataaatatgtttctctgttcaacgaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agccaaagttcattctgctaagatacacaagcatccagtctcagaaactttaaaagaggc 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                        cryptica
                                                                                                                                                                                                                                                                                                                                   cryptica uppl gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.6%;
nilarity 51.4%;
Conservative
Roessler PG;
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                             96US-0627873
                                            96US-0627873
                                                                                                        /number= 3
147°
                                                                                                                                                   /*tag= e
/number= 2
886 .1402
                                                                                                                                                                                                                             /*tag- b
/number- 1
                                                                                                                                                                                               315..782
                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                     /number-
                                                                                                                                                                          783..885
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                                                                                                                                                                                                                      25..314
                                                                                                                                                                                                                                                  /note- "contains introns"
                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                            403..1478
                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                           *tag=
                                                                                                      479..3640
                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                    3640
                                                                                                                                                                                                                                                                                                            upp1; UDP-glucose pyrophosphorylase; UDPase; PGMase; multifunctional enzyme; lipid; sugar;
                                                                                                                                                                                                                                                                                                                                                                                3640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 30.8;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503
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This sequence corresponds to the tobacco (Nicotiana tabacum) anthranilate synthase gene ASA2. The gene's promoter and DNA constructs containing it are useful for imparting, to a plant cell, tolerance to an amino acid analogue of Trp, or altering the Trp content in a plant by transforming the plant cells with an expression cassette containing the ASA2 structural gene. The promoter and construct are useful for the production

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RESULT
Z30444
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Best Local
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                                                                                                                     WPI; 1999-579943/49.
P-PSDB; Y41301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the uppl gene from Cyclotella cryptica which encodes a multifunctional enzyme with both UDP-glucose pyrophosphorylase (UGPase) and phosphoglucomutase (PGMase) activities. The enzyme may be used to modulate the amount of lipid, carbohydrate and sugar produced by organisms.
                                                                  Claim
                                                                                                Plant tissue culture transformation using
                                                                                                                                                  Widholm JM,
                                                                                                                                                                                                                                                                                                                                  Tobacco
                                                                                                                                                                                                                                                                                                                                                      18-JAN-2000
                                                                                                                                                                    (UNII ) UNIV
                                                                                                                                                                                        26-JUL-1996;
25-JUL-1997;
                                                                                                                                                                                                                      31-DEC-1997;
                                                                                                                                                                                                                                          12-OCT-1999.
                                                                                                                                                                                                                                                                                 Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                   tryptophan;
                                                                                                                                                                                                                                                                                                           Promoter; tobacco; anthranilate synthase; tolerance;
                                                                                                                                                                                                                                                                                                                                                                          230444;
                                                                                                                                                                                                                                                                                                                                                                                            Z30444 standard; DNA; 2161 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           2454 ttgttgaggtgatcccctcgac 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2394 ttgacataactcaagtcggagctaccactgttgcagccgctgatggaagtacaagtgttg 2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3640 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a protein from Cyclotella cryptica, useful for modulating the lipid or carbohydrate content of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-429508/36.
P-PSDB; Y24308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 TTGAAACAACTGAATTTGGCGCTTACTTTGCGACACCCGCTGATGATACTTTACGTTTTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATTGGCGCAATCGCTACGGC 146
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                                                                  Column
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                                                                                                                                                                                                                                                                                                   transgenic plant;
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                  Brotherton
                                                                                                                                                                      ILLINOIS FOUND
                                                                                                                                                                                        96US-0025140.
97US-0937739.
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                                                                  29-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.6%;
                                                                                                                                                                                                                                                                                                                                 synthase
                                                                  49pp; English.
                                                                                                                                                  JE,
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                                                                                                                                                 Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.8;
Pred. No. 9
                                                                                                                                                                                                                                                                                                     SS
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                                                                                                                                                                                                                                                                                                              analogue;
                                                                                                  DNA
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V52138/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mNNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide
                                                                                                                                                                                                                                                                           Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae genome fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V52138 standard; DNA; 13926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1264 tgcagatgttaaaagatgagaaacaacgcgcagagca
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                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                pneumoniae
                                                                                                                                                                                                                                                                                                                                          WPI; 1998-272225/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09818931-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V52138;
                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 TGTTTATTTCAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gaccactggctgggacaagcagaagagggaagacacctgatgaggatgtgatgttggaaa 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGCGGTCGCTGGGACAAGCCGGCGCGCGGGACGGATGGCGCTGACGATATCGCGTTAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttttagttgcatcgagcccagaaattttgacacgtgtgaagaagaagaagaattgttaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCGTTGTTAGCCAGTCAGAAAAACCGCATTGAACA
                                                                                                                                                                                                                               1; Page 174-182; 1409pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2161 BP; 603 A;
                                                                                                                                                                                                                                                                                                                                                                       Rosen
                                                                                                                                                                                                                                                                                                                                                                                     Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0029960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US19588
                                                                                                                                                                                                                                                                                                                                                                       CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.6%;
49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                   SCI INC
                                                                                                                                                                                                                                                                                                                                                                                     Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 C; 530 G; 608 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. pneumoniae; genome; diagnosis; as
vaccine; pharmaceutical composition;
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                     Dougherty BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2161;
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
1662 AGTTGGTTGGAACAGGATCCCAAAAATCGCTCTGAAAATATGATGATTGTGG
                                                                                                                                                                1782
                                                                                                                                                                                                                                            1842 AATCGTATGGTGGTAGAGCAGGAGGCGGGCTACAATGCCTATGTGGAACATGACGAGATG 1783
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13926 BP; 3889 A; 2986 C; 2460 G; 4591 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragments of the S. pneumoniae genome. Products from invention can be used in diagnosis kits and assays, a compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S. pneumoniae genome of commercial importance, or expression modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                  571 TTGTTTATTTCAGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACG
                                                                                                                                                                                                                                                                                511 ATTCGTGCGTTAGCTGAGCAGGCGAATACGTATCATGTGGTTTTAAAGCGACATGATGAA 570
                                     GAAGCGTTGTTAGCCAGTCAGAAAAACCGCATTGAACATCAATATGTCGTGG 742
                                                                              CGACCAATGAAGGGGACGACTCAGCGTGGGGGTAACTGACCAAGAAGATCTTGAACAGGCC
                                                                                                                 GCGGCGGTCGCTGGGACAAGCCGGCGCGCGGGACGGATGGCGCTGACGATATCGCGTTAGGC
                                                                                                                                                              ACAGTGATTTCCATGAGCCCAGAGCTCTTTTTTGAGCAAAATGATCGCGAGTTGACAACA
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                           2.5%;
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                             Score 30.4;
Pred. No. 28;
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pharmaceutical
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Search completed: November Job time: 3907 sec 25, 2000, 02:08:35

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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/1/ina/6_COMB.seq:*
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US-09-001-826-25
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US-09-101-826-25
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US-07-854-5968-18
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US-08-774-104A-1
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GENERAL INFORMATION:
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TITLE OF INVENTION: RECOMBINANT N-SMASES
TITLE OF INVENTION: ENCODING SAME
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CORRESPONDENCE ADDRESS:
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5164490-2 US-08-792-832A-47	US-08-570-311-25 US-08-369-043-1 US-09-356-952-12	US-08-808-599A-1 US-08-141-324-13 US-08-541-902-13	US-08-317-522A-1 US-08-439-818A-1 US-08-751-965-1 US-08-738-975-1 US-08-728-626-1	US-09-041-991A-3 US-08-454-196-16 US-09-064-033-16 US-07-723-002C-3 US-08-309-512-1 PCT-US92-08756A-1
47,	25, 1, A	13,7	,,,,,,	Sequence 3, Appli Sequence 16, Appl Sequence 16, Appli Sequence 3, Appli Sequence 1, Appli

ALIGNMENTS

AND NUCLEIC ACIDS

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; MOLECULE TYPE: ci
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-774-104A-1
                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 12/24/96
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1197 base pairs
                                                                                                                                                                                                                       TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                               TOPOLOGY:
                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                         TELEPHONE: 617-523-34
TELEFAX: 617-523-6440
                                                                                                                                                                                                                                                      NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 469
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GAGAAGACACCTCGTGGCTTGTTTGCAGGTCCTATTGGCTATTTTACCGCAGATAATAGT
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GAGCAGGCGAATACGTATCATGTGGTTTTAAAGCGACATGATGAATTGTTTATTTCAGCA 585

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RESULT 2
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Matches 14
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: (703)836-9300
                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION.
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUMBER OF SEQUENCES:
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STREET: 18
CITY: Alex
STATE: VA
COUNTRY: U
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                   TELEFAX:
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1800 Diagonal Road,
                                                                                                                                                                                                                     (703)683-4109
                2.8%;
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; Score 33.8; DB Pred. No. 0.43; 203; Mismatches
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US-08-088-633-1
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                                                                                                                                                                           TELEPHONE: (619)552-131
TELEFAX: (619)552-0095
TELEX: 20 6566 PATLAW (
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/678,916
FILING DATE: 01-APR-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  NAME: Reiter, Stephen E
REGIESTION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619,552-1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1130
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2032 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Ev
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: unkn
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SYSTEM: PC-DOS/MS-DOS
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Bradley D
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RESULT 4
US-08-245-756-1
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US-08-245-756-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
1.FNGTH: 2032 base pairs
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Best Local S
Matches 71
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APPLICANT: Gleeson, M
APPLICANT: HOWARD, Br
TITLE OF INVENTION: G
TITLE OF INVENTION: A
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/67
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COMPUTER: PC-
COMPUTER: Patentin R
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COMPUTER: PATENTIN DAT
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                                                                                                                                                                                                                                                                                                                FILING DATE: 01-APR-1991
ATTORNEY/AGENT INFORMATION:
                                              FEATURE
                                                                                            FEATURE:
                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: unkn
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1
CLASSIFICATION:
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nes 71; Conserv
                             NAME/KEY:
                                                                             NAME/KEY:
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                                                             LOCATION:
                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                      NAME:
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                                                                                                                            unknown
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SYSTEM: PC-DOS/MS-DOS
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239..1468
              mat_peptide
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                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                               Stephanie
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Bradley D
GENES WHICH INFLUENCE PICHIA PROTEOLYTIC
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Best Local Sim
Matches 71;
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                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,756
FILING DATE: 16-May-1994
                                                 MOLECULE TYPE:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                         FILING DATE: 01-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-May-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                   FEATURE:
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APPLICATION NUMBER:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                        NAME: Seidman, Stephanie REGISTRATION NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 9763
                                                                                 TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/08 FILING DATE: 06-JULY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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Similarity 51.4%;
71; Conservative
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GENES WHICH INFLUENCE PICHIA PROTEOLYTIC
ACTIVITY, AND USES THEREFOR
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US-08-441-750-1
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US-08-441-751-1
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Best Local Similarity 51.4
71; Conservative
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                                                                         TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                        NAME: Seidman, Stephanie REGISTRATION NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 970 TELECOMMUNICATION INFORMATION: 619-238-0999
                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/088,633
                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/08
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                            FILING DATE: 01-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                  TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/2/
FILING DATE: 16-May-1994
                                                            LENGTH:
                                                                                                                                                                                                                            APPLICATION NUMBER: 07/6 FILING DATE: 01-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                              H: 2032 base pairs nucleic acid
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239..1468
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Best Local Similarity 51.4%;
Matches 71; Conservative
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TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/678
FILING DATE: 01-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2032 base pairs
                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)552-1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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ADDRESSEE: Fitch, Ev
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                 FEATURE:
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                                                                               MOLECULE TYPE:
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                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME/KEY:
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135 South LaSalle Street, Suite 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gleeson, Martin A
Howard, Bradley D
WENTION: GENES WHICH INFLUENCE PICHIA PROTEOLYTIC
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mat_peptide
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Pred. No. 2.1;
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Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                         TELEFAX: 303/384-7499
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROESSLEY, INTITLE OF INVENTION: IS TITLE OF INVENTION: PHOTOLOGY OF INVENTION: CY
                                                                                                                                                                                                                                                                                                                      NAME: Edna M. O'Connor
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII(DOS)text (*.*)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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MOLECULE TYPE:
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STREET: LC
CITY: Golden
'ms: CO
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                                                                                            FEATURE:
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                                            NAME/KEY:
LOCATION:
NAME/KEY:
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FILING DATE: April 3, 1996
CLASSIFICATION: 435
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80401-3393
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303/384-7499
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Pred. No. 2
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; Sequence 25, Application US/09001826A
Patent No. 5965727
; GENERAL INFORMATION:
: APPLICANT: SONG, HEE-SOOK
: APPLICANT: BROTHERTON, JEFFREY E.
: APPLICANT: WIDHOLM, JACK M.
: TITLE OF INVENTION: SELECTABLE MARKER AN
: TITLE OF INVENTION: TRANSFORMATION
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US-09-001-826-25
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US-09-001-826-4
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Best Local S
Matches 78
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Best Local S
Matches 50
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LENGTH: 2161
TYPE: DNA (CDNA)
ORGANISM: Nicotiana tabacum
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APPLICANT: SONG, HEE-SOOK
APPLICANT: SONG, HEE-SOOK
APPLICANT: HOPHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
FILE REFERENCE: UI001.Cl
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CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Macintosh Wordperfect converted to PC ASC: TABLE: Macintosh Wordperfect converted to PC ASC: M
                                                                                                                                                                                                                                                                                                                                                                                                                        1264 tgcagatgttaaaagatgagaaacaacgcgcagagca
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LOCATION:
NAME/KEY:
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mes 50; Conservative
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1479..3637
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Pred. No. 3;
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                                          AND PROMOTER
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CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 458
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR TITLE OF INVENTION: RECEPTOR PROTEINS FILE REFERENCE: 19999Y
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TYPE: DNA (cDNA)
ORGANISM: Nicotiana t
FEATURE:
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CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
NUMBER OF SEQ ID NOS: 31
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TYPE: PRT
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278
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                                    844 ATTACAGGGGACATTGCGGCACATTTAAGTGTGACCGCGATTGTTGACCGCTTGCATCCA 903
                                                                            338 MS.H.HK.RHHTRB..H..S.SYRBBC....KWTS...SK.HT.S.AS.C..DMTWC..
                                                                                                                                                           398 T.D.BH..M.BT.BH..DKSHSNT.T.TM.AB...M..MKSMRMMB....TNN.H..CT.
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                                                                                                                                                                                                                                                                                      664 GATGGCGCTGACGATATCGCGTTAGGCGAAGCGTTGTTAGCCAGTCAGAAAAACCGCATT 723
BB..YHT.HG.AA.TM.HSH.BA.H.KTR.M...TB..DSB.MNR.MMT..B...N.R.S 219
                                                                                                                                                                                                                                         BMT..K...MDK.BMC..M.NR.D.BTMASA.Y...AK.KMCTYY.H.KD.CT.RH.. 399
                                                                                                                  AAGGTGCCGGCCATGCCAAGTTTACTCAAAAATAAGCAAGTTCAGCATTTGTACACACCA 843
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Pred. No. 1.1;
95; Mismatches 193;
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0; Mismatches 79;
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Pred. No. 2.
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US-08-242-098-39
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Best Local Similarity 51.1%;
Matches 69; Conservative
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Patent No. 56911
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/133,390
FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Lactic Acid Bacterial Suppressor Mutants
TITLE OF INVENTION: and Their Use as Selective Markers and as Means of
TITLE OF INVENTION: Containment in Lactic Acid Bacteria
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                     188 CGCAGTCATTTGATG 202
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                                                                                                                                                                                   68 AAACAACTGAATTTGGCGCTTACTTTGCGACACCCGCTGATGATACTTTACGTTTTGGCA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/242,098 FILING DATE: 13-MAY-1994
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                    TTGGCGCAATCGCTACGGCAAAAACGGCTCAGGCATTACAAGGTGCGGTTGTTTTTGGTG 187
                                                                TTAAAGCAGGTCTTGCAGAAAATATGGTTCCAGAATCAGCAACTGCAGTGATTTCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                            1419 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Foley & Lardner 3000 K Street, N.W., Suite 500 ashington, D.C.
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(202)672-5399
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HANSEN, Egon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           39:
                                                                                                                                                                                                                          Score 29.4; DB Pred. No. 5.1; 0; Mismatches
                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                 Length 1419;
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US-08-572-951-3
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CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text
SEQ ID NO 24
LENGTH: 1650
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Applicati Patent No. 5824790 GENERAL INFORMATION:
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APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE TITLE OF INVENTION: TRANSFORMATION FILE REFERENCE: UI001.C1
  ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           APPLICANT: KNIGHT, MARY E.
APPLICANT: GUAN, HANPING
TITLE OF INVENTION: MODIFIC
TITLE OF INVENTION: SYNTHE:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     582 AGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCGGCGGTCGC
                                                                                                                                             STREET: 1100 New CITY: Washington STATE: DC
                                                                                                                                                                                 ADDRESSEE: CUSHMAN DARBY & CUSHMAN ADDRESSEE: Intellectual Property Group o: ADDRESSEE: Pillsbury Madison & Sutro LLP STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 96; Conserv
                                                                                                    COUNTRY: USA
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agagaatgaaaagcaaagtgctgagca 948
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PatentIn Release #1.0,
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Pred. No. 5.6;
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Mismatches 111;

0; Gaps

0

641

921

DB 4;

Length 1650; Indels

Version #1.25

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RESULT 15
US-08-846-762-1
US-08-846-762-1
; Sequence 1, Application US/08846762A
; Patent NO. 5994072
; Patent NO. 5994072
; PAPELICANT: Lam, JOSeph S.
; APPLICANT: Lam, JOSeph S.
; APPLICANT: Charter, Deborah
; APPLICANT: Ge Klevit, Teresa
; TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
; FILE REFERENCE: 6580-089
; FILE REFERENCE: 6580-089
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                                                                                                        ; LENGTH: 24417
; TYPE: DNA
; ORGANIZM: Pseudomonas aeruginosa
US-08-846-762-1
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Query Match
Best Local Similarity 51.1
Matches 69; Conservative
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                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/572,951
FILING DATE: 15-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,602
FILING DATE: 29-NOV-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2380 base pairs
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APPLICATION NUMBER: 08/263
FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Paul N. Kokulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: bot
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1604 GNTTYATHGGNMGNYTNGAYCAYCAR 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1544 GYAARGCNGCNYTNCARMGNCARYTNGGNYTNCARGINMGNGAYGAYGTNCCNYTNATHG 1603
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         2.5%; Score 29.4; I
51.1%; Pred. No. 30;
ative 0; Mismatches
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ER: 222957/1.02.15C
                                             DB 4;
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           66;
                                             Length 24417;
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Search completed: November 25, 2000, 01:48:46 Job time: 20709 sec

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Title:
Perfect score:
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Gapop 10.0 , Gapext 1.0
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1 ATGATGACATATCACGAAAC.....ACTACAATCATGTCGAATGA
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Copyright (c) 1993 - 2000
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gb_est5:
gb_est7:

                                                        9b_est10:
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ACCESSION VERSION KEYWORDS SOURCE

AW398687 638 bp mRNA EST 07-FEB-2000
EST309187 L. pennellii trichome, Cornell University Lycopersicon
pennellii CDNA clone cLPT4016 5', mRNA sequence.
AW398687
AW398687.1 GI:6917157
EST.
Lycopersicon pennellii.
Lycopersicon pennellii.
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ORGANISM

DEFINITION

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AUTHORS

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21 CNS016N4
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C71727 C71727 Rice
AI993966 70149494
AI997116 70155212
AV549266 AV549266
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AV540872 AV560872
AV370802 MTBA38B12
BB345415 BB345415
BB345415 BB345415
BB3535242 BB535242
AQ824936 HS_5283 A
BB535242 BB373760
BB203673 BB303673
W90867 mf79e05.r1

FEATURES

prime sequence.

ocation/Qualifiers

source

/organism="Lycopersicon pennellii"
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/clone="cLPT4016"
/clone_lib="L. pennellii trichome, C.
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"

Cornell University"

O 0.0

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Result

Description

JOURNAL COMMENT

Contact: David trichomes Unpublished (1999)

Frisch

Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 4366 Fax: 864 656 4293 Email: dfrisch@CLEMSON.EDU

SC 29634, USA

TITLE

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I. Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fuji ,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin ,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from wild tomato (Lycopersicon pennellii)

Holt,I.E. B., Fujii

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases I to 638)

ALIGNMENTS

BB210443 AW829046 AQ305162

3 BB210443 6 ra33d03.y 2 HS_2019_B 0 AA17F09 A

BE038450

RESULT AW398687

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ALO53013 Drosophil AALO5313 VEM-1a3-u AQ047433 CLM-1a3-u AW582990 ia08g11.y D48678 RICS15048A ALO69204 Drosophil BB325541 BB325541 AI648665 tx63g12.x AQ916714 nbeb0067E AL106973 Drosophil AI008381 EST202832 AQ418315 RPC1-11-1

/note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoI; Leaves of various stages were shaken in liquid nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."

126 c 164 g 169 t

882
Db 468 ATTTCAACATCTTTACGCTCGATTGAGGGGGAGACTCCCAGGCTGAAGATGATCATTTAA 527
QY 822 AGTTCAGCATTTGTACACACCAATTACAGGGGACATTGCGGCACATTTAAGTGTGACCGC 881
Db 408 GGAGGCTGTGTTCAAGCGTTATAATTGAACCAAAGAAAGCAATAAGAAAATTTACAAG 467
Qy 762 GCAAGACGTCGACGACGTCGCTAAAGGTGCCGGCCATGCCAAGTTTACTCAAAAATAAGCA 821
Db 348 ATCCAGCGCTAAGGACCATAATGAGTTTGCTATAGTACGGGAGTGCATAAGAAGAAGAATT 407
Qy 702 AGCCAGTCAGAAAAACCGCATTGAACATCAATATGTCGTGGCAAGTATCACGACACGCTT 761
Db 288 TGGAACACGGGCTAGGGGTGGATCAGAGCTTCTGGATCTTAATATAGAACATGATTTACT
Qy 642 TGGGACAAGCCGGCGGGACGGATGGCGCTGACGATATCGCGTTAGGCGAAGCGTTGTT 701
Db 228 AACACCTCCAGAGCAGCTATTTCATCGGGACCGCCTCAGCATTTGTAGTGAGGCTTTAGC
QY 582 AGCAACACCGGAACGGTTAGTGGCTATGTCAGGTGGTCAGATCGCTACGGCGGCGGTCGC 641
Hest Local Similarity 45.5%; Pred. No. 1.7e-05; Matches 187; Conservative 0; Mismatches 224; Indels 0; Gaps
Query Match 4.4%; Score 52.6; DB 22; Length 638;

AL266099 Tetracodon C08171 C08171 Yuji AV189838 AV189838 AW351559 IL2-CT003 AW216289 687047E01 AW850622 IL3-CT021 BB540703 BB540703 C36520 C36520 Yuji BB540703 BB540703 C36520 C36520 Yuji BB378305 BB378305 BB233297 BB233297 D71830 CELK082C8R BB210509 BB210509

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann R., Waterston, R., and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: estéwatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 195.
    Location/Qualifiers
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200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer [GACAGAGAGAGAGAGAGAGTCTCCAG(T)].BV] to anchor the primer at the 5' end of the poly(A) tract. After second strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoR1 adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI from Promega (40Vul); all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 8-day-old 'Williams' seedlings which were propagated on paper towels with distilled water for 3 days (etiolated), then greenhouse grown for 5 days in potting soil. The cotyledons were flash-frozen in liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Cotyledons of 8-day-old·/Williams/
seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1032-1703"
/clone_1ib="Gm-c1032"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               itrogen. Stratagene's cDNA Synthesis Kit (catalog number 00401) was used to synthesize the cDNA. First-strand
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                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                95148729
On Jan 7, 1998 this sequence version
                                                                                                                                                                                                 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                   Tel: 517-353-0854 Fax: 517-353-9168
                                                                                                              Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
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                                                           Lansing,Mi
                                                                            MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                    Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                 thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
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22313tcn@ibm.cl.msu.
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Pred. No. 0.00053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTTTNATTAAGGAGATAGAATCATTCGATAGAGGAATNTATGCGGGACCTATTGGATT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C71727 457 bp mRNA EST 22-SEP-1997 C71727 Rice panicle at flowering stage Oryza sativa cDNA clone E0143_1A, mRNA sequence.
C71727 C71727.1 GI:2427264
                                                                                                                                                                                                                                                       Sasaki,T. and Yamamoto,K.
Rice cDNA from panicle at flowering stage
Unpublished (1996)
Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 457)
                                                          Email: tsasaki@abr.affrc.go.jp.
Location/Qualifiers
1. .457
                                                                                                                                                                                                            National Institute of Agrobiological Resources Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
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a 61 c 107 g
/strain="Nipponbare"
/db_xref="taxon:4530"
                                  /organism="Oryza sativa"
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/clone="111A12T7"
/clone_lib="Lambda-PRL2"
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Pred. No. 0.0032;
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896 TGCATCCAACACCAGCACTGGGTGGCGTCCCACGTGAAGCGGCCCTGTATTACATTGCGA 955

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701494994 A. thallana, Ohio State cl
CDNA clone 701494994, mRNA sequence.
A1993966
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                                                                                                                                                                                                                                                                                                              Pharmaceuticals, Inc.
4633 World Parkway Circle,
Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                   Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                    Contact: David Smoller, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
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Location/Qualifiers
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/clone_lib="Rice panicle at flowering stage"
/dev_stage="flowering stage"
/note="Organ: panicle; Rice cDNA from panicle
stage"
                                                                                                          /clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones'
Arabidopsis thaliana Ohio State clone set."
1 141 c 78 g 154 t
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/db_xref="taxon:3702"
/clone="701494994"
                   3.3%;
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                 Score 39.6; DB Pred. No. 0.21;
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TTGGCATTGGCGCAATCGCTACGGCAAAAACGGCTCAGGCATTACAAGGTGCGGTTGTTT 181
                                                   CATCTCANNNNNNNNNNNNNNNNNNNNNATGTTCCTGCACTAAGTGATGCTTTGACTC 334
                                                                     CACTTGAAACAACTGAATTTGGCGCTTACTTTGCGACACCCGCTGATGATACTTTACGTT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                            94;
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701552128 A. thaliana,
CDNA clone 701552128, n
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                                                                                                                        Similarity 45.
94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 service@genomesystems.com
Location/Qualifiers
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                                                                                                                                                                                                                         library was derived from untreated root tissue from Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks. Plants were grown in 1:1:1 peat moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C under constant light, and watered with fertilizer. cDNA synthesis was initiated using a NotI-oligo(dT) primer. Double-stranded cDNA was blunted, ligated to SalI adaptors, digested with NotI, size-selected, and cloned into the NotI and SalI sites of the pSPORT vector."

119 c 91 g 145 t 22 others
                                                                                                                                                                                                                                                                                                                                                                                                    /clone_11b="A. thaliana, Columbia Col-0, root-2"
/tissue_type="root"
/dev_stage="4 - 7 weeks"
/note="Vector: pSPORT; Site_1: NotI; Site_2: SalI; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
/clone="701552128"
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/cultivar="Columbia Col-0"
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Pred. No. 0.57
0; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                         22 CATCTCAAGCAACAACAACAACCAATGTTCCTGCACTAAGTGATGATGCTTTGACTC 81
                                                                                                                                                                                                                                                                                                                                                                                                                               62 CACTTGAAACAACTGAATTTGGCGCTTACTTTGCGACACCCGCTGATGATACTTTACGTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                        GGTTTGTCCCCGAAGTGATGGTGACCA 268
                                                                                                                                                                                                  TTTGTGTGGATGCACCATCTGAAGCAGTGTGTGTGCCCGTGTGGACATGTCGCCGGATGCA 201
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                                                                                                                                                                                                                              TTGGTGCGCAGTCATTTGATGAACAAGAGTACCCGCAGTCTGAATTGATGGCGGGTTTTT 241
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                                                                                                              TTTCTTGCTTGAAAGAGATTGAAAACA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 7, 175-180 (2000)
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A large scale analysis of cDNA in of 12,028 non-redundant expressed size-selected cDNA libraries
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Eukaryota; Viridiplantae;
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AV560872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                              TTTCTTGCTTGAAAGAGATTGAAAACA
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                                                                                                                                                                                                sequence.
AL370502
                                                                   Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for Plant Gene Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-081
Email: asamizu@kazusa.or.jp, URL:htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
             1 (bases 1 to 439)
Journet, E.P., Crespeau, H., van Tuinen, D., Gouzy, J., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gian.
                                                                                                                                                                                                                                 MtBA38B12F1 MtBA Medicago
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                                                                                                                                           barrel medic.
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Contact: Erika Asamizu
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Gamas, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="SQ141h12F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tlssue_type="green siliques"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
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                                                                                                                                                     AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 CGATGAGGAAGTTGAAGGTGCTGAAGATGATGCATCCTTAGTCAAACACATTGGTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 CTATGCGGCACTTGAAACAACTGAATTTGGCGCTTACTTTGCGACACCCGCTGATGATAC 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTTGTTTTTGGTGCGCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCCGGTTTTCCGCAGTCGAGTCCAAACGGGAAGATCAAATTCAAGCTGCTCATGATGA 344
I (bases 1 to 280)

Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata
                                                                                                                                                                                                                                                                                                                                                musculus
BB345415
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BB345415
                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 / hasas 1 +> 2000
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Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                   EST
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BP 191 91006 EVRY cedex - France
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissuc_type="root tips"
//tissuc_type="root tips"
//dev_stage="harvested after 3 days of N-starvation"
//note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; PLAnts were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                                                                                                                                                                                                                                                                                                                                                                     280 bp mRNA EST 12-
RIKEN full-length enriched, 10 days neonate
cDNA clone B930056M08 3', mRNA sequence.
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/clone="MtBA38B12"
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/oultivar="Temalong"
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182 ATAACATTGACACAACTGCCAAGAGACCTCCTGGCGTATACTTTAGTGTTGCTTAGTATT 241
                                                    944 ATTACATTGCGACCCATGAGAAGACACCTCGTGGCTTGTTTGCAGGTCCTATTGGCTATT 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
                                                                                                           l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sciences Center
3-1-1 Koyadai, Tsukuba,
Tel: +81-298-36-9013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba
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Unpublished (2000)
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URL:http://genome.rtc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                   prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                  Vector: a modified pBluescript KS(+) after bulk
from Lambda FLC I. Cloning sites, 5' end: Sall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cerebellum"
/dev_stage="10 days neonate"
/lab_host="DH10B"
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                                                                                                                                 Score 36; DB
Pred. No. 2.3;
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JOURNAL
                                                                                                                                                                          Matches
                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                           398 AACGGACAGAGAATTTGATTGATAGCCTTAGCCATCGATCAAACCTTAGCCAAAGTCGTTT 457
                                          458 TTGGTCGGCAACAGACCCTGCAGTTATCCGACACGTTACGACTGGCACAAATTATT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 TGACTGCTAATGATAGTGAAGATCTTCTGGTT 273
  70
AATTGAAATAGAATTTCATTACCTCCTCTGCTGTAGATAAGCTCTTATCCAAAGTTTTCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetic/s (info@res.gen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 420 row: N column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-420N16.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Nierman,W., Feldblyum,T.,
,B., Levins,M., Mcgann,S., Tsegaye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 382)
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RPCI-23-420N16.TV RPCI-23 Mus musculus genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                             EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 44\ c 87 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                selected DNA was cloned into the pBACe3.6 vector at the
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/clone="RPCI-23~420N16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
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56.9%;
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Pred. No. 2.5;
0; Mismatches 50;
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clone RPCI-23-420N16
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RESULT 12
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashlzaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninoi,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
y and Hayashizhiy.
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BB535242 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030042I18 3' similar to L06421 Murine
trombospondin 2 mRNA, exon 22 (3'UTR), mRNA sequence.
BB535242
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Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +81-298-36-9013
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.rtc.riken.go.jp) for
                              /note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                         RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                               /dev_stage="0 day neonate"
/lab_host="DH10B"
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/clone="E030042I18"
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trehalose thermo-activated reverse
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1078 ACTITATITGCTGGTGCCGGGATTGTGGCTGACTCCGATGCGCAACAAGAATATGAAGAA 1137
                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTTATTTGCTGTTGATGATCTTTGGTATAAAAATGAAGCTCTAGCTGAATGAGGGGTT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pleter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 859 row: M column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ824936 525 bp DNA GSS 2:
HS_523A1_G07_SP6E RPCI-11 Human Male BAC Library |
genomic clone Plate-859 Col=13 Row=M, DNA sequence.
AQ824936 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scanning the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                   BAC ends
                  and partially digested with a combination of ECORI Methylase. Size selected DNA was cloned pBACe3,6 vector at ECORI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 56\ c 28\ g 91\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Male blood DNA was isolated from one randomly chosen
                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                            /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
                                                                                                                                   /sex="male"
                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                     Location/Qualifiers
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57.7%;
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RPCI-11 Human Male BAC Library Homo sapiens
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BB552509/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATAAACATATGCTGTATCGTTTCACGATGATTATGAGGTACATTAGTGATCTGAACAG 340
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                                                                                                                               Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
In Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashia,Vi.
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,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)
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Mammalia; Eutheria;
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RESULT 15
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Local Similarity 56.4%;
Konno, H. Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hoti, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Kayosawa, T., Maki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Singemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
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/lab_host="DH10B"
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URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishlyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Nuramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
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Carninci,P. and Hayashizaki,Y.
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/dev_stage="16 days embryo"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130071N21"
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SUMMARIES

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CC A host cell containing a vector comprising a nucleotide sequence

CC encoding N-SMase can be used to produce N-SMase. N-SMase can be used in

CC a method for identifying a compound useful in the diagnosis or treatment

CC of a human neutral sphingomyelinase related disorder. N-SMase, and a

CC nucleotide sequence encoding N-SMase, can be used for modulating N-SMase

CC caltvity, and for treating a disorder associated with N-SMase. The

CC N-SMase disorders that can be treated with the nucleotide sequence or

CC N-SMase, is an inflammatory disorder, arthritis, osteoarthritis, Crohn's

CC disease, obesity, diabetes, cirrhosis, susceptible tumours, central

CC nervous system disorder, vascular restenosis, arterial occlusion arising

CC from plaque formation, cardiac disease where LV dysfunction occurs,

CC hypercholesterolaemia, cholesteryl ester storage disorder, renal failure,

CC HIV infection, depression, schizophrenia, neurodegeneration, and

CC Alzheimer's disease. An antibody against N-SMase can be used to reduce

CC cells
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         Isochorismate synthase; ICS; plant; pathogen resistance; pathogen inducible promoter; antipathogenic protein; toxi antifungal protein; albumin-type protein; hypersensitive
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Alzheimer's disease
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                                                                                                                                                                                                                                                          FAGAGIVADSDAQQEYEETGLKFEPMRQLLKDYNHVE
                                                                                                                                                                                                                                                                                                     TPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRATL
                                                                                                                                                                                                                                                                                                                                                                                                                            HVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAQSFDEQEYPQSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gaqsfdeqeypqselmagfwfvpevmvtiaadkitfgsdtvsdfttwlaqfvpkqpntvt
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Pred. No. 8.6e-181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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03-APR-1998;
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(UYLE-) RIJKSUNIV LEIDEN.
(UYNI-) UNIV NIJMEGEN.
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vgffggaqs-dfsvgirsaligk-dagaliyaglgvvegsdpalewqelelkasqfmklm
                                                   IGYFTADNSGEFVVGIRSMYVNQTQRRATLFAGAGIVADSDAQQEYEETGLKFEPMRQLL
                                                                                                                              NKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGP
                                                                                                                                                                                                                                                                                     {\tt arrsqvittsdidplawlssfkadgkdayqfclqpheapafigntpeqlfgrdqltvfse}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGAQSFDEQEY -- PQSELMAGFWF - VPEV ----- MVTIAAD -----
                                                                                                  {\tt lkriqhlyarfagrlrseddefkilsslhptpavcgfpmedarkfiaenemfdrglyagp}
                                                                                                                                                                                           alaatrargesdsldlqmahdlfsspkdnhefaivrenirqkldaictsvetepmksvrk 454
                                                                                                                                                                                                                                        AVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTTSLKVPAMPSLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                      ITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWIERTENLIDTLAIDQT-LAKVVF 152
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Melchers LS,
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Pred. No. 1.
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Croes AF,
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                                                                                                                                                          Query Match
Best Local S
Matches 113
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98US-0080625
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28.6%;
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Bol
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                                                                                                                                                              65;
                                                                                                                                                                                               Score 344; DB 20;
Pred. No. 2.9e-24;
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Croes AF, S
JF;
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                                                                                                                                                          Gaps
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RESULT
Y33698
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                                                                                                                                                                                                                                                                                                                                                   Isochorismate synthase; ICS; plant; pathogen resistance; chitinase; pathogen inducible promoter; antipathogenic protein; toxin; entC; antifungal protein; albumin-type protein; hypersensitive response,
                                                                                                                                                      Simons
                                                                                                                                                                                                                                     31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                    25-MAR-1999;
                                                                                                                                                                                                                                                                                          07-OCT-1999
                                                                                                                                                                                                                                                                                                            WO9950423-A2
                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Y33698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y33698 standard; Protein; 271 AA
                                                                                                    Method
                                                                                                                                                                Van
                                                                                                                                                                          Linthorst HJM,
                                                                                                                                                                                             (UYNI-)
                                                                                                                                                                                                       (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
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                                                                                                                                                               Tegelen
                                                                                                                                 1999-610856/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQTQRRATLFAGAGIVADSDAQQEYEETGLKFEPM : | | | | | | | | | | | | | | |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERTENLIDTLAI-DQTLAKVVFGRQQTLQLS---DTLRLAQIIRALAEQANTYHVVLKR-: |:|: | : | : | :|:|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rengvr--lfagagivpassplgewretgvklstm
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                                                                                                                                                                                              UNIV
                                                                                                  inducing pathogen resistance
                                                                                                                                                    Melchers
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98US-0080625
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                                                                                                                                                               Verpoorte, Wullems
                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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                                                                                                                                                                                                                                                                                                                                                                                            fragment.
                                                                                                                                                     B G, R
                                                                                                                                                   Verberne MC,
Croes AF, S
JF;
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This invention describes a novel method for the induction of pathogen resistance in plants, by transformation with an expression cassette harboring a gene coding for an isochorismate synthase (ICS). A pathogen inducible promoter can be used to drive expression of a heterologous protein. The heterologous protein used in the method of the invention is an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins, as a natipathogenic protein e.g. chitinase, glucanase, osmotin, lectins,

toxins

is

Example

3; Page 53-54; 66pp;

English.

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RESULT
Y50336
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thuringiensis, or antifungal proteins isolated from Mirabilis jalapa, Amaranthus, Raphanus, Brassica, Sinapis, Arabidopsis, Dahlia, Cnicus, Lathyrus, Clitoria, Allium seeds, Aralia and Impatiens and albumin-type proteins, such as thionine, napin, barley trypsin inhibitor, cereal gliadin and wheat-alpha-amylase, or a protein that can induce a hypersensitive response, such as Cf, Bs3 and Po proteins from tobacco. This sequence encodes the Escherichia coli isochorismate synthase entC gene which is described in the method of
            WPI;
N-PSDB;
                                                                                                                                           31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                Isochorismate synthase; ICS; plant; pathogen resistance; chitinase; pathogen inducible promoter; antipathogenic protein; toxin; antifungal protein; albumin-type protein; hypersensitive response.
                                                                                                                                                                                                                                                                                                                                  P. fluorescens ICS orfA protein
                                                                                                                                                                                                                                                                                                                                                              14-JAN-2000
                                                             Linthorst HJM,
                                                                                                                                                                                25-MAR-1999;
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                                                                                                                                                                                                                                                        Psuedomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                             Y50336 standard; Protein;
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                                                Van Tegelen
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                                                                                                     (UYLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 IRALAEQ---ANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDI : | | | : : : : | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 QFVPKQPNTVTTSHVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQI
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            1999-610856/52
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                                     H,
                                                                                      MOGEN INT NV.
RIJKSUNIV LEIDEN.
UNIV NIJMEGEN.
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91; Conservative
                                    n LJP, Wul
Melchers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 AA;
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                                                                                                                                         98US-0080203
98US-0080625
                                                                                                                                                                               99WO-EP02176
                                                             Verpoorte
                                              Wullems
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                                     , ST
                                    GJ,
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                391 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 329.5; DB 2
Pred. No. 3.9e-23;
16; Mismatches 124
                                                Verberne MC,
Croes AF,
                                                 Stuiver MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
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                                                              Moreno
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                                                Custers
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC Inducible promoter can be used to drive expression of a heterologous conducible promoter can be used to drive expression of a heterologous conducible promoter can be used to drive expression of a heterologous conducible promoter can be used to drive expression of a heterologous contains. The heterologous protein used in the method of the invention is contained exidase, oxalate exidase, magainins, toxins from Bacillus thuringiensis, or antifungal proteins isolated from Mirabilis jalapa, containingiensis, or antifungal proteins isolated from Mirabilis jalapa, containingiensis, or antifungal proteins isolated from Mirabilis jalapa, containingiensis, or antifungal proteins solated from Mirabilis jalapa, containingiensis, or antifungal proteins solated from Mirabilis jalapa, containingiensis, containingiensis, Arabidopsis, Dahlia, Cnicus, containingiensis, Allium seeds, Arabid and Impatiens and albumin type proteins, such as thionine, napin, barley trypsin inhibitor, cereal contains, such as thionine and the protein that can induce a hypersensitive response, such as Cf, Bs3 and po proteins from tomato and Contain from tobacco. This sequence represents the Pseudomonas contains and such as Sochorismate swithers orfa norfain which is decorated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                          Isochorismate synthase; ICS; plant; pathogen resistance; pathogen inducible promoter; antipathogenic protein; toxi antifungal protein; albumin-type protein; hypersensitive
                                                                                                      P. fluorescens
                                                                                                                                         14-JAN-2000
                                                                                                                                                                               Y50338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e evqlaevqrs fs fts gdrelavtg \verb|mlqrietpaiggddans| fqqtiaqaldrare agq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEYPQSELMAGFWFVP --- - EVMVTIAADKITF --- - GSDTVSDFTTWLAQ -----
                                                                                                                                                                                                                                                                                                      sspdsewaevqtk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISATPERLYAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ravehavvnfrhsdvrkavlsvqrelifandvdvsalqhnlkaqnpsgyhfrvpmpdgtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTLAKVVFG-----RQQTLQLSDTLRLAQIIRALAEQANT-----YHVVLKRHD-EL
                                                                                                                                                                                                                                                                                                                                                                           erarrlirfvepferglftgmvgwcdaqgngewvvtircgtvrrnkvr--lfagagivea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snpiivgaipfdpaepscl---yipehaqwrtrdihaktgmstlpelieqknipdeqafk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducing pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                        (first entry)
                                                                                                      ICS
                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                          382
                                                                                                    orfA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.1%;
28.7%;
                                                                                                                                                                                                                  331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 302.5; DB 2
Pred. No. 2.3e-20;
                                                                                                                                                                                                                B
                                                                                                  fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                 chitinase;
                               response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ġaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                308
                                                                                                                                                                                                                                                                                                                                                                             366
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Psuedomonas fluorescens

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RESULT
Y41302
ID Y4
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel method for the induction of pathogen resistance in plants, by transformation with an expression cassette harboring a gene coding for an isochorismate synthase (ICS). A pathogen inducible promoter can be used to drive expression of a heterologous protein used in the method of the invention is an antipathogenic protein e.g. chitinase, glucanase, osmotin, lectins, saccharide oxidase, oxalate oxidase, magainins, toxins from Bacillus thuringlensis, or antifungal proteins isolated from Mirabilis jalapa, Amaranthus, Raphanus, Brassica, Sinapis, Arabidopsis, Dahlia, Cnicus, Lathyrus, Clitoria, Allium seeds, Aralia and Impattens and albumin-type proteins, such as thionine, napin, barley trypsin inhibitor, cereal gliadin and wheat-alpha-amylase, or a protein that can induce a hypersensitive response, such as Cf. Bs3 and Po proteins from tomato and Protein in from tobacco. This sequence represents a Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1998;
03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9950423-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              fluorescens isochorismate synthase orfA protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for inducing pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Van Tegelen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linthorst HJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYNI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999;
                                                                                                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                         234
                                                                   292
                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                   PNTYTTSHVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRAL-A 174
                                                                                                                                                                                                                                   qnpsgyhfrvpmpdgttligvspellvrkeglsslsnplagsakrmadpeadrrnadwll
                                                                                                                                                                                                                                                             EQANTYHVVLKRHD-ELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALL
                                                                                                                                                                                                                                                                                       pelieqknipdeqafkravehavvnfr-hsdvrkavlsvqrelifandvdvsalqhnlka
                                                                                            QTQRRATLFAGAGIVADSDAQQEYEETGLK 382
                                                                                                                     qlacrlhptpavcgfpterarrlirfvepferglftgmvgwcdaqgngewvvtircgtvr
                                                                                                                                     tsekdhyehgfvtqdivsqlgklctqlnvpqrpslistpalwhlstriegtladpavsal
                                                                                                                                                                                                      ASQKNRIEHQYVVASITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITGDIA-AHLSVT
                                                                   rnkvr--lfagagiveasspdsewaevqtk 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LH,
                                                                                                                                                                                                                                                                                                                                                87;
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                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Page 58-59; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IJM, Verpoorte H
1 LJP, Wullems (
Melchers LS, H
                                                                                                                                                                                                                                                                                                                                                Conservative
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98US-0080625
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                                                                                                                                                                                                                                                                                                                                                            14.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GJ,
Bol
                                                                                                                                                                                                                                                                                                                                             ; Score 297; DB 2; Pred. No. 6e-20; 43; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Verberne MC,
Croes AF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuiver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plants
                                                                                                                                                                                                                                                                                                                                                134;
                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moreno
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment which
                                                                                                                                                                                                                                                                                                                                                                        Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MH,
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Custers
                                                                                                                                                                                                                                                                                                                                                6,
                                                                                                                                                                                                                                                                                                                                               Gaps
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Y41302 standard;

Protein;

491

Y42112 ID Y' XX

Y42112 standard; Protein;

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Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                       This sequence corresponds to the tobacco (Nicotiana tabacum) anthranilate synthase ASA1. The corresponding gene's promoter and DNA constructs containing it are useful for imparting, to a plant cell, tolerance to an amino acid analogue of Trp, or altering the Trp content in a plant by transforming the plant cells with an expression cassette containing the ASA2 structural gene. The promoter and construct are useful for the production of transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5965727-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant tissue culture transformation using promoters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Widholm JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1996;
25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophan; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Promoter; tobacco; anthranilate synthase; tolerance; analogue; Trp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNII ) UNIV
                                                                                                                                                                                                                                                              110
                                   418
                                                           343
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                                                                                                                                                           225
                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                      Local Similarity 26.4 nes 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-579943/49.
DB; Z30446.
                                   alslrtivfptacqyntmysykdankrrewvaylqagagvvadsdpqdehce
                                                             VVGIRSM-----
                                                                                                 GDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEF
                                                                                                                                                          DIALGEALLASQKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPIT
                                                                                                                                                                                  evyralrvv--npspymgylqargcilvasspeiltkvkqnkivnrplagtskrgkneve
                                                                                                                                                                                                            RLAQIIRALAEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGAD
                                                                                                                                                                                                                                    qfgpsldn----snvtce----eykeavvk--akehilagdifqivlsqrferrtfadpf 240
                                                                                                                                                                                                                                                             QFVPKQPNTVTTSHVTDEVDWIERTENLIDTLAIDQTLAKVVF - - - - - GRQQTLQLSDTL
                                                                                   gelqdgltcwdvlraalpvgtvsgapkvkamelideleptrrgpysggfggvsftgdmdi
                                                                                                                                   dkrl-eellenekqsaehimlvelgrndvgkvtkygsvkveklmnieryshvmhisstvt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Column 41-44; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                   491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brotherton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILLINOIS FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0025140
97US-0937739
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                                                                                                                                                                                                                                                                                                 10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JE,
                                                         YVNQTQRR---ATLFAGAGIVADSDAQQEYEE 378
                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                    Pred. No. 2e-1
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Song
                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                 209;
No.
                                                                                                                                                                                                                                                                                                   2e-11;
                                              DB
                                                                                                                                                                                                                                                                                      123;
                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    • _
                                                                                                                                                                                                                                                                                      36;
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                                                                                                                                                           282
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P Vo B 68 68

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SXCCCCCCCCCCCCCCCCCCCCCX by proving a superior of the superior
                                                                                                                                                                                                                           The present invention describes isolated anthranilate synthase alpha-
CC subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan
CC synthase alpha-subunit (TSAS) nucleic acids, and protein encoded by them,
CC obtained from corn, rice, Soybean and wheat cDNA libraries. The nucleic
CC acid fragments may be used to create transgenic plants in which the
CC disclosed ASAS, ASBS or TSAS are present at higher or lower levels than
CC normal or in cell types or developmental stages in which they are not
CC normally found. This would have the effect of altering the level of
CC tryptophan in those cells. Manipulation of the levels of some of the
CC ASASs will also results in changes in the response to pathogen attack.
CC Because this pathway is not followed for the production of tryptophan in
CC higher animals, these enzymes are very good candidates for the discovery
CC of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as
CC targets to facilitate design and/or identification of inhibitors of those
CC enzymes that may be useful as herbicides. Nucleic acid fragments can also
CC to used as probes for genetically and physically mapping the genes that
CC they are a part of, and as markers for traits linked to those genes. Such
CC with desired phenotypes. Z25109 to Z25127 represent specifically claimed
CC nucleic acids from the present invention and Y42112 to Y42130 represent
                                 Query Match
Best Local (
            Matches
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated tryptophan biosynthetic enzyme nucleic acids, used to produce plants with altered tryptophan levels and for developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthranilate synthase alpha subunit; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       produce plants with alter
herbicides or fungicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rafalski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vollmer SJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn anthranilate synthase alpha subunit protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1999
                                    Local Similarity
                                                                                                                                                                                                               proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Page 55-57; 83pp;
      61;
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                                                                                                                                                        603 AA;
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Falco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US06046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SC,
                                 9.7%;
26.5%;
                                                                                                                                                                                                            by them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Broglie
      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                              Score 195.5; DB 20; Pred. No. 5e-10;
      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bryan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GT,
      105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cahoon
      Indels
                                                         Length
      19;
Gaps
```

04 B 64

254

84

Local

Similarity

9.7%;

Score 195; DB 20; Pred. No. 5.7e-10;

Length 616; Indels 3

Conservative

69;

Mismatches

141;

34;

Gaps

٥

140 TLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANTYHVVLKRHDELFISATPERL 199

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Sequence
                                                                  the
                                                                                         an
by
                                                                                                         an amino acid analogue of
                                                                                                                                                    This sequence corresponds to the tobacco (Nicotiana tabacum) anthranilate synthase ASA2. The corresponding gene's promoter and DNA constructs
                                                                                                                                                                                                                                                                                    Plant tissue culture transformation using promoters
                                                                                                                                                                                                                                                                                                                                                                                               Widholm JM,
                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-579943/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1996;
25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5965727-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco anthranilate synthase ASA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2000
                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tryptophan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter; tobacco; anthranilate synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y41301 standard; Protein; 616
                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNII ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 slrtivfstapshntmysykdadrrrewvahlqagagivadsspddeqre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
                                    nthase ASA2. The corresponding gene's promoter and DNA constructs ntaining it are useful for imparting, to a plant cell, tolerance to amino acid analogue of Trp, or altering the Trp content in a plant transforming the plant cells with an expression cassette containing e ASA2 structural gene. The promoter and construct are useful for the oduction of transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIRSM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt lddhlqswdalraalpvgtvsgapkvkamelidklevtrrgpysgglggisfdgdmqial}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mqeqqllsdekqcaehimlvdlgrndvgkvskpgsvkveklmnieryshvmhisstvsgq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGEALLASQKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evyralrivnpspymayvqargcvlvasspeiltrvskgkiinrplagtvrrgktekedq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QIIRAL-AEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDI 226
                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                  Column 31-34; 49pp; English.
616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic
                                                                                                                                                                                                                                                                                                                                                                                                  Brotherton
                                                                                                                                                                                                                                                                                                                                                                                                                                           ILLINOIS FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0025140
97US-0937739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0001826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----YVNQTQRR----ATLFAGAGIVADSDAQQEYEE 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant
                                                                                                                                                                                                                                                                                                                                                                                                  JE,
                                                                                                                                                                                                                                                                                                                                                                                             Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                               Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tolerance; analogue;
                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                    DNA constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  530
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RESULT W93814
ID W93
AC W93
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вb
맑
                                                                                                     Matches
                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                        This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encodes ^a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HOKK
NORQ
                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09911800-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice anthranilate synthase second isozyme alpha-subunit protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W93814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W93814 standard;
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304
     354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
                                              168 QIIRAL-AEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-228982/19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THEKTPRGLFAGPIGYFTADNSGEFVVGIRSM---
evyralrivnpspymayvqargcvlvasspeiltrvrkgkiinrplagtvrrgktekede 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sgagivadsnpdeeqie 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGIVADSDAQQEYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gsvnveklmsveryshvmhisstvsgelldhltcwdalraalpvgtvsgapkvkamelid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOKKO
JAPAN
                                                                                                  Similarity 26.
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Η,
                                                                                                                                                                                                                                                                                                                                                                                                  Page 139-141;
                                                                                                                                                                                                                            909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Terakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN AGRIC FORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tryptophan content; nutritional value
                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97JP-0235049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-JP03883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                         9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                               152pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORESTRY & FISHERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tozawa
                                                                                               Score 189.5; DB 2
Pred. No. 1.8e-09;
5; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y,
                                                                                                  102;
                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVNQTQRR---ATLF
                                                                                                                                                 Length
                                                                                                                                                 606;
                                                                                                  23;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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В
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Y42113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
      The present invention describes isolated anthranilate synthase alphaces subunit (ASAS), anthranilate synthase beta-subunit (ASBS), and tryptophan cypy synthase alpha-subunit (TSAS) nucleic acids, and protein encoded by them, cobtained from corn, rice, soybean and wheat cDNA libraries. The nucleic acid fragments may be used to create transgenic plants in which the collicity of in cell types or developmental stages in which they are not normal or in cell types or developmental stages in which they are not commally found. This would have the effect of altering the level of tryptophan in those cells. Manipulation of the levels of some of the ASAS will also results in changes in the response to pathogen attack. Because this pathway is not followed for the production of tryptophan in those crimes are very good candidates for the discovery of herbicides and fungicides. The ASAS, ASBS or TSAS can be used as complete that may be useful as herbicides. Nucleably manipulation that can also be used as manipulation and or manipulation of inhibitors of those cargines that may be useful as herbicides. Nucleably manipulation that the constant was also that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chimeric gene; corn; rice; soybean; wheat; tryptophan biosynthetic enzyme; chimeric gene; corn; rice; soybean; wheat; tryptophan synthase; anthranilate synthase beta subunit; herbicide; fungicide; phenotype; pathogen attack; identification; transgenic plant; ASAS; ASBS; TSAS; plant breeding.
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                Vollmer SJ,
Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn anthranilate synthase alpha subunit portion protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                            21; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Falco
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This protein sequence comprises a maize anthranilate synthase (AS) that is resistant to inhibition by free L-tryptophan or its amino acid analogues. Its amino acid sequence was deduced from a cDNA
                                                                                                             Claim 4; Fig 7; 87pp; English.
                                                                                                                                                                                                                                                                                         WPI; 1997-385350/35.
N-PSDB; T91102.
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                                                                                                                                                                      DNA encoding anthranilate synthase resistant to inhibition by tryptophan - and transformed plants, used e.g. to improve try levels in plants and as marker for cell selection
                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                          Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize C28 allele anthranilate synthase alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                              (DEKA-) DEKALB GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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26.1%;
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Pred. No. 2.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
           N-PSDB;
                       WPI; 1997-385350/35
                                                    Anderson
                                                                                                                                                                                                                                                                                                                                                           Maize anthranilate synthase alpha subunit
                                                                                                                                                                                                                                                                                                                                                                                                                     W26686;
                                                                                                              19-JAN-1996;
                                                                                                                                                                       24-JUL-1997.
                                                                                                                                                                                                    WO9726366-A1
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                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                               Anthranilate synthase; L-tryptophan; tolerance; transgenic plant; maize; selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998
                                                                                  (DEKA-) DEKALB GENETICS CORP
                                                                                                                                           17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                W26686 standard; Protein; 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 lslrtivfstapshntmysykdadrrrewvahlqagagivadsspddegre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 QIIRAL-AEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGIRSM-----YVNQTQRR---ATLFAGAGIVADSDAQQEYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qlddhlqswdalraalpvgtvsgapkvkamelidklevtrrgpysgglggisfdgdmqia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mqeqqllsdekqcaehimlvdlgrndvgkvskpggsvkvekl-iieryshvmhisstvsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALGEALLASOKNRIEHQYVV---ASITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evyralrivnpspykayvqargcvlvasspeiltrvskgkiinrplagtvrrgktekedq 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
                                                     PC,
                                                                                                                                                                                                                                                                                    inbred line Va26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                     Chomet PS,
                                                                                                              96US-0604789
                                                                                                                                         97WO-US00983
                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                            /label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.2%;
26.0%;
                                                     Griffor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 184.5; DB 1 Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 105;
                                                     S.
                                                     Kriz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18;
                                                     AL;
                                                                                                                                                                                                                                                                                                                                 resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
W9381.5
ID W9381.5
VXX W9381.5
VXX Z2
VXX Z2
VXX Z2
VXX Z2
VXX XX
VXX Z2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants to Trp analogues; (ii) to alter, particularly increase, the Trp content of plants, either to increase nutritional value or as a source of Trp by extraction; (iii) for production of recombinant AS (used for screening to identify agents that bind to or inhibit it); and (iv) for selection of transformed cells. Transgenic plants containing AS can be used for production of proteins or other compounds, including in vitro culture of their cells. The trait of
                                                                                                                                                                                                                                                 W09911800-A1
                                                                                                                                                                                                                                                                                               Oryza
                                                                                                                                                                                                                                                                                                                                               maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the alpha subunit (see W26685) of a maize allele C28 AS that is resistant to inhibition by free L-tryptophan or its amino acid analogues. Maize AS sequences, especially those from the C28 allele, can be used in claimed methods: (1) to impart tolerance of
                                                                                                                                                                                                11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                       Anthranilate
                                                                                                                                                                                                                                                                                                                                                                                                                          Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W93815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W93815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                       (HOKK ) HOKKO CHEM IND CO LTD. (NORQ ) JAPAN MIN AGRIC FOREST
                                                                                                 29-AUG-1997;
                                                                                                                                               31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance to Trp can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               levels in plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding tryptophan -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inbred line Va26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                                                                                                                                                                                                                                                                                                                  ASA first isozyme alpha-subunit protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lslrtivfstapshntmysykdadrrrewvahlqagagivadsspddegre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VGIRSM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evyralrivnpspymayvqargcvlvasspeiltrvskgkiinrplagtvrrgktekedq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIIRAL-AEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qlddhlqswdalraalpvgtvsgapkvkamelidklevtrrgpysgglggisfdgdmqia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mqeqqllsdekqcaehimlvdlgrndvgkvskpggsvkvekl-iieryshvmhisstvsg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGEALLASQKNRIEHQYVV----ASITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit
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                                                                                                                                                                                                                                                                                                                                               wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                       synthase; alpha-subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded
                                                                                                                                                                                                                                                                                                                                             tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ã,
                                                                                                 97JP-0235049.
                                                                                                                                               98WO-JP03883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transformed plants, used e.g. to and as marker for cell selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ence comprises a maize anthranilate synthase oded by a cDNA clone (see T91103) obtained fit differs at only 1 residue (Met 377 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in vitro culture of their cells. The trait of
be introduced to a wide variety of commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YVNQTQRR---ATLFAGAGIVADSDAQQEYEE
                         FORESTRY
                                                                                                                                                                                                                                                                                                                                             content; nutritional value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 183.5; DB 1
Pred. No. 6.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                         B
                       FISHERIES
                                                                                                                                                                                                                                                                                                                                                                       ASA;
                                                                                                                                                                                                                                                                                                                                                                 rice; isozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase (AS btained from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615;
                                                                                                                                                                                                                                                                                                                                                                 plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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RESULT
W93810
ID W93810
AC W9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                (HOKK )
                                                                    WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthase - used for improving tryptopha nutritional value of crops, e.g. rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encodes ^a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and
                                                                                                                                      Hasegawa H,
                                                                                                                                                                                                                                                    29-AUG-1997;
                                                                                                                                                                                                                                                                                               31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                        WO9911800-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthranilate synthase; alpha-subunit; ASA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice anthranilate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W93810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W93810 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isozyme alpha-subunit.
transformant plants an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                           11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 alrtivfptgsrfdtmysytdknarqewvahlqagagivadskpddehqe
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                                                                    1999-228982/19
DB; X23748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGEALLASQKNRIEHQYYVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGD
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yme alpha-subunit. The encoding DNA can be used to produce
sformant plants and seeds, of e.g. rice, maize or wheat, with
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DB; X23754.
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                                                                                                                                                                                HOKKO
JAPAN
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25.7%;
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                                                                                                                                      Tozawa
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Pred. No. 9.
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4.

DNA encodes ^a-subunit of first isozyme c synthase - used for improving tryptophan

first isozyme of rice anthranilate

production

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Search completed: November 25, 2000, 02:17:00 Job time: 3222 sec
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                                                                                                                                                                                                                                                                                                                   Query Match 9.0%; Score 181.5; DB 20; Length 577; Best Local Similarity 25.7%; Pred. No. 9.7e-09; Matches 59; Conservative 45; Mismatches 107; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 128-131; 152pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nutritional value of crops, e.g. rice, maize or wheat
                                                                                                                                                                                                                                                      345 GIRSM-----YVNQTQRR---ATLFAGAGIVADSDAQQEYEE 378
                                                                                                                                446 lrddltcwdalraalpvgtvsgapkvramelidqmegkmrgpysggfggvsfrgdmdial 505
                                                                                                                                                 285 IAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVV 344
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Listing first 45 summaries
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MMTYHETRALAQSDLQQLYA.....ETGLKFEPMRQLLKDYNHVE 397
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US-08-604-789B-2
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US-08-910-505-2
US-08-910-505-2
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US-08-910-505-2
US-08-78-7640-2
US-08-78-7640-2
US-08-78-7640-2
US-08-78-785-081-5
PCT-US95-0894-5
US-08-78-785-759-7
US-08-712-709-8
US-08-712-709-1
US-08-715-769-1
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Subr Subr DDIN Steil Set Sion: S/08 S/08 S/08 S-2: S-2: S-2: S-2: S-33,88 SR: ODIN	123222123111 4 13
us/08774104A e. Subroto ENCOMBINANT N-SMASES AND NUCLEIC ENCODING SAME 7 S: S: Tronstein, Roberts & Cushman, LLP Street M: M: Atthe atible DOS Version 1.5 ATA: US/08/774,104A /96 /96/08/774,104A /96 /96/08/774,104A /96 MMBER: 46906 ORMATION: -3400 4440 NO: 2: 1CS: acids ile iin minal	US-08-913-581-4 US-08-237-919-2 PCT-US95-05518-2 US-08-433-854-4 US-08-174-745A-4 US-08-195-947-4 US-08-433-908B-4 US-08-433-908B-4 US-08-548-509-5 US-08-548-509-2 US-08-614-377A-7 US-08-542-003-2 US-08-673-814-6 US-08-673-814-6 US-08-689-756-1 US-08-418-893D-23
ACIDS	Sequence 4, P. Sequence 2, P. Sequence 4, P. Sequence 4, P. Sequence 4, P. Sequence 5, P. Sequence 5, P. Sequence 7, P. Sequence 2, P. Sequence 1, P. Sequence 1, P. Sequence 1, P. Sequence 2, P. Sequence 2, P. Sequence 2, P. Sequence 1, P. Sequence 1, P. Sequence 2, P. Sequence 3, P. Sequence 2, P. Sequence 2, P. Sequence 2, P. Sequence 2, P. Sequence 3, P. Sequence 2, P. Sequence 2, P. Sequence 3, P. Sequence 4, P. Sequence 3, P. Sequence 4, P. Sequence 3, P. Sequence 3, P. Sequence 4, P. Sequence 4, P. Sequence 5, P. Sequence 5, P. Sequence 6, P. Sequen
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Query Match

100.0%;

Score 2009;

DB 2;

Length 397;

100.0%;

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US-08-604-789B-3
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           INFORMATION
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                                                                                                                    COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
PRIOR APPLICATION NUMBER: «Unknown»
FILING DATE: CUnknown»
FILING DATE: CUnknown»
APPLICATION NUMBER: «Unknown»
FILING DATE: CUnknown»
ATTORNEY, ACENT INFORMATION:
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                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, L
STREET: P.O. Box 2938
CITY: Minneapolis
STATE: MI
STATE: MS
                                     TELEFAX: (612) 339-3061
                                                                                                                                                                                                                                                                              ZIP: 55402
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Anderson, P.C. Chomet, P.S.
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMTYHETRALAQSDLQQLYAALETTEFGAYFATPADDTLRFGIGAIATAKTAQALQGAVF
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                                                                                REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
             TELEX: <Unknown>
                                                                                                             NAME: Woessner, Warren D.
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffor, M.C.
Kriz, A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                           OVERPRODUCTION
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                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 31
SOFTWARE: Macintosh Wordperfect converted to PC ASCII SEQ ID NO 23
LENGTH: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23, Applica Patent No. 5965727 GENERAL INFORMATION:
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 77; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,
EARLIER FILING DATE: 1997-07-25; 1996-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 QFVPKQPNTVTTSHVTDEVDWIERTENLIDTLAIDQTLAKVVF-----GRQQTLQLSUTL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OFVPKQPNTVTTSHVTDEVDWIERTENLIDTLAIDQTLAKVVF-----GRQOTLQLSDFL 164
                                 DIALGEALLASOKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPIT 282
                                                                      EVYRALRVV--NPSPYMGYLQARGCILVASSPEILTKVKQNKIVNRPLAGTSKRGKNEVE
                                                                                                                                      QFGPSLDN----SNVTCE----EYKEAVVK--AKEHILAGDIFQIVLSQRFERRTFADPF 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKRLEKELLENEKQCAEHIMLVDLGRNDVGKVTKYGSVKVEKLMNIERYSHVMHISSTVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLAQIIRALAEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGAD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QFGPSLDN----SNVTCE----EYKEAVVK--AKEHILAGDIFQIVLSQRFERRTFADPF 343
DKRL-EELLENEKQSAEHIMLVELGRNDVGKVTKYGSVKVEKLMNIERYSHVMHISSTVT
                                                                                                       RLAQIIRALAEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGAD 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELQDGLTCWDVLRAALPVGTVSGAPKVKAMELIDELEPTRRGPYSGGFGGVSFTGDMDI
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                10.4%;
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                                                                                                                                                                                                                                  Score 209;
Pred. No. 1
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                                                                                                                                                                                                                    Mismatches
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l.8e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124;
                                                                                                                                                                                                                                                   Length 491;
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HOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-08-604-789B-4
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US-08-604-789B-4
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Patent No. 6118047
GENERAL INFORMATION:
APPLICANT: Anderson, P.C.
                                                                                                                                                                                            Matches
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                            169
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                                     361 ALRIV--NPSPYMAYLQVRGCILVASSPEILLRSKNRKITNRPLAGTVRRGKTPKEDLML
229 GEALLASQKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGDIA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
TELEFAX: (612) 339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Woessner, Warren D.
                                                                        IIRALAEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALSLRTIVFPTACQYNTMYSYKDANKRREWVAYLQAGAGVVADSDPQDEHCE 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GELQDGLTCWDVLRAALPVGTVSGAPKVKAMELIDELEPTRRGPYSGGFGGVSFTGDMDI
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                                                                                                             FGPKLEKSTWTSEAYKEA-VVEAKEHILAGDIFQI-----VLSQRFERRTFADPFEIYR 360
                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 621 amino acids
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, P.C. Chomet, P.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffor, M.C. Kriz, A.L.
                                                                                                                                                                                      10.0%; Score 201.5; DB 3; 24.0%; Pred. No. 1.6e-12; tive 56; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OVERPRODUCTION
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -YVNQTQRR----ATLFAGAGIVADSDAQQEYEE
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                                                                                                                                                                                                                             Length 621;
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RESULT 6
US-08-604-789B-16
; Sequence 16, Application US/08604789B
; Patent No. 6118047
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Macintosh Wordperfect converted to PC ASCII Text SEQ ID NO 5
LENGTH: 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SONG, HEE-SOOK
APPLICANT: BROTHERTON, JEFFREY E.
APPLICANT: WIDHOLM, JACK M.
TITLE OF INVENTION: SELECTABLE MARKER AND PROMOTER FOR PLANT TISSUE CULTURE
TITLE OF INVENTION: TRANSFORMATION
FILE REFERENCE: UI001.C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/001,826A
CURRENT FILING DATE: 1997-12-31
EARLIER APPLICATION NUMBER: 08/937,739; 60/025,140
EARLIER FILING DATE: 1997-07-25; 1996-07-26
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                              542
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                                                                                                                                                                                                                                                                              THEKTPRGLFAGPIGYFTADNSGEFVVGIRSM-
                                                                                                                                                                                                                                                                                                                                                                                                    TRVKKRRIVNRPLAGTSRRGKTPDEDVMLEMQMLKDEKQRAEHIMLVDLGRNDVGKVSKP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                          VAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIAAGDIFQIVLSQRFERRTFADPFEVYRALRIV--NPSPYMTYIQARGCILVASSPEIL
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                                                                                                                                                           SGAGIVADSNPDEEQIE
                                                                                                                                                                                                                                                                                                                     GSVNVEKLMSVERYSHVMHISSTVSGELLDHLTCWDALRAALPVGTVSGAPKVKAMELID 481
                                                                                                                                                                                                                                                                                                                                                           -SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIA 317
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Pred. No. 7.6e-12;
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                                                                                                                                                                                                                                                                              -YVNQTQRR---ATLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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APPLICANT: Anderson, P.C. Chomet, P.S.

Griffor, M.C.

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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-604-789B-16
                                                                                                                                                          RESULT 7
US-08-604-789B-2
                                                                                                  Sequence 2, Application Patent No. 6118047 GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                          471
                                                                                                                                                                                                                                                                                                                                                                                                        412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352
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                                                                                                                                                                                                                                           531 LSLRTIVFSTAPSHNTMYSYKDADRRREWVAHLQAGAGIVADSSPDDEQRE 581
                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                                                                         227 ALGEALLASOKNRIEHQYVV----ASITTRLODVTTSLKVPAMPSLLKNKQVQHLYTPITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, WARTEN D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/604,789B
FILING DATE: 19-Jan-1996
                                   APPLICANT: Anderson, P.C.
Chomet, P.S.
Griffor, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTHRANILATE SYNTHASE GENE
AND METHOD OF USE THEREOF FOR CONFERRING TRYPTOPHAN
OVERPRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            DIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFV 343
                                                                                                                                                                                                                                                                                                                                                                                                      MQEQQLLSDEKQCAEHIMLVDLGRNDVGKVSKPGGSVKVEKL-IIERYSHVMHISSTVSG
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                                                                                                                                                                                                                                                                                                                        QLDDHLQSWDALRAALPVGTVSGAPKVKAMELIDKLEVTRRGPYSGGLGGISFDGDMQIA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60;
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TOPOLOGY: linear
TULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MN
  ဓ္
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITY: Minneapolis
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INVENTION: ANTHRANILATE SYNTHASE GENE
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                                                                                                                                         US/08604789B
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-08-604-789B-2
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US-09-320-878-4
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Best Local S
Matches 60
                                                                                                                                                                     Sequence 4, Application US/09320878A Patent No. 6117659
                                                                                                                                                  GENERAL INFORMATION:
                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (612) 339-3061
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 amino acids
TYPE: amino acid
STRANDEDNESS: single
APPLICANT: TANG, L1
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
                                                                                        APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352
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                                                                                                                                                                                                                                                                                                                     344 VGIRSM------YVNQTQRR---ATLFAGAGIVADSDAQQEYEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.026US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WOESSNEY, Warren D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-Jan-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman,
STREET: P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                              DIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVYRALRIVNPSPYMAYVQARGCVLVASSPEILTRVSKGKIINRPLAGTVRRGKTEKEDQ 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                     McDANIEL, Robert
TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/604,789B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 183.5; DB 3
Pred. No. 1.2e-10;
5; Mismatches 105
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CURRENT APPLICATION

NUMBER: US/09/320,878A

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PCT-US95-06994-8
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; ORGANISM: Streptomyces venezuelae
US-09-320-878-4
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                                                                                                                                                                                                                                                                                                                         Sequence 8, Applicati
GENERAL INFORMATION:
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Best Local Similarity
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SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/087,080 EARLIER FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28
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                                                                                                                                                                 APPLICANT: TARR, PHILLIP I
APPLICANT: BILGE, SIMA S
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                         APPLICANT:
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                 COUNTRY: USA
ZIP: WA 98101
                                                                         STREET: SUITE CITY: SEATTLE
                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TYHETRALAQSDLQQ-LYAALETTEFGAYFATPADDTLRFGIGAIATAKTAQALQGAVFG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LDRVDVVQPV----TFAVMVSLAKVWQHHGITPEAVIGHSQGEIAAAYVAGALTLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAMEHRAVAVGDSREALRDALRMPE-GLVRGTVTDP-----GRVAFVFPGQGTQWAGMG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRGTDGADDIALGEALLASQKNRI------EHQYVVASITTRLQDVTTSL--KVPA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAARVVTLRSKSIAAHLAGKGGMISLALSE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQSFDEQEYPQSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/100,880 FILING DATE: 1998-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1999-05-
                                                                                                                                                                                                                                                                                                                                           Application PC/TUS9506994
                                                       WASHINGTON
                                                                                           E: CHRISTENSEN, C
SUITE 2800, 1420
                                                                                                                                                                                                                                                                 Children's Hospital & Medical Center
University of Washington
Washington State University Research
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24.2%;
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                                                                                           O'CONNOR, JOHNSON AND KINDNESSPLLO
O FIFTH AVENUE
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                                                                                                                                                                                                                                                                   Research Foundation
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                                                                                                US-09-320-878-2
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             GENERAL INFORMATION:
APPLICANT: ASHLEY,
APPLICANT: BETLACH,
                                                                Patent No.
                                                                            Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local S
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 APPLICANT:
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ORIGINAL SOURCE:
ORGANISM: Esch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 24-JUN-1994 ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                           459
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                                                                                                                                                                                                                                                                                                                                                                                                                                               123 HVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANTYHV.182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 QRYDNRDGQLGSLTGGY----DRTLRYERNKISAGYDGTFTFGTWKSY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: in DESCRIPTION: SI POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 QSFDEQEYPQSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESCRIPTION:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                 DALALTAGSRYEHHEQFGGHFSPRAYLVWDVADAWTLKGGVTTGYKAPRMGQLHKG----
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                                                             Application 6117659
 BETLACH,
BETLACH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                 ASHLEY, Gary
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E. coli 0157:H7 adhesin amino acid sequence, wherein "Xaa" residues represent gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        introduced to facilitate SEQ ID NO:9.
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Melanie C.
Mary C.
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                                                                              US/09320878A
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                                                                                                                                                                                                                                                                                                                   ------YVVASITTRLQDVTTSLKVPAMPSLLKNKQVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                           502
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RESULT 11
US-08-910-505-2
Sequence 2, Application US/08910505A
Patent No. 6107071
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                                                                                                       GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Marti
APPLICANT: Hodgson, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 2
                                                                    APPLICANT:
APPLICANT:
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Best Local (
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EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
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TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
                                   APPLICANT:
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EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
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 APPLICANT:
                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                         LGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGE 341
                                                                                                                                                                                                                                                                                                                                                            VPFFSTLEGAWITEPALDGGYWYRNLRHRVGFAPAVETLATDEGFTHFVEVSAHPVLTMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAARVVTLRSKSIGAHLAGQGGMLSLALSE-----AAVVERLAGFDG--LSVAAVNGPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D----TLRLAQIIRALAEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTS
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                                                                    Knowles, David
Nicholas, Richard
 Ward,
                                 Pratt, Julie
Reichard, Raymond
                                                                                                         Burnham, Martin
Hodgson, John
Rosenberg, Martin
Ward, Judith
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Pred. No.
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; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-910-505-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-910-505-4
                                                                                                                                                                                                                                         APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Julie
APPLICANT: Reichard, Raymond
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
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SEQ ID NO 2
TOUGHH: 416
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                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                           APPLICANT: Lonetto, Michael
APPLICANT: Warren, Pattick
TITLE OF INVENTION: NOVEL HISTIDINOL DEHYDROG
FILE REFERENCE: P50549-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/910,505A
CURRENT FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                  CURRENT APPLICATION NUMBER: US/08/910,505A CURRENT FILING DATE: 1997-08-04
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APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL HISTIDINOL DEHYDROG
FILE REFERENCE: P50549-02
                                                                             NUMBER OF SEQ
                                                                                                                                                                                                                               APPLICANT: Ward, Judith
LENGTH: 416
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
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                                                                                 ID NOS:
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; ORGANISM: Staphylococcus aureus US-08-910-505-4

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                                                           ; ORGANISM: Streptomyces venezuelae US-09-320-878-3
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US-09-320-878-3
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Best Local Similarity
                                                                                                                                             SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/087,080 EARLIER FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/100,880 EARLIER FILING DATE: 1998-09-22
                                                                                                    LENGTH: 15
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
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  Score 92.5;
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Length 1562;
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Query Match

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MOLECULE TYPE: HYPOTHETICAL:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 20.3 Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                 TELEFAX: 908-594-4720 INFORMATION FOR SEQ ID NO:
                                                                                                               REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VINCI, VICTOR A.
APPLICANT: CONDER, MICHAEL J.
APPLICANT: MCADA, PHYLLIS C.
                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ZIP: 07065-0907
                                                                                                                                                                   NAME: CARTY, CHRISTINE REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 25-MAY-1995
TOPOLOGY:
              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VWQHH-----GITPQAVVGHSQGEIAAAYVAGALTLDDAARVVTLRSKSIAAHLAGKGG
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                                               3038 amino acids
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ROMITON: DNA ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REEVES, CHRISTOPHER DAVIS, CHARLES R. HENDRICKSON, LEE E.
                                                                                                   908-594-4720
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linear
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6 E. LINCOLN AVENUE, P.O. Box 2000
               single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-637-640-2
; Sequence 2, Application US/08637640
; Patent No. 5849541
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Best Local Similarity
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APPLICANT:
APPLICANT:
                            APPLICATION NUMBER: US/08/637,6
FILLING DATE: 23-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/148,132
FILING DATE: 01-NOV-1993
                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: NAME: CARTY, CHRISTINE E.
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                     APPLICANT: RAMBOSEK, JOHN
TITLE OF INVENTION: DNA ENCODING TRIOL POLYKETIDE SYNTHASE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CITY: R
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                                                                                                                                                                                                                                                                                    ADDRESSEE: CHRISTINE E. CARTY
STREET: P.O. BOX 2000; 126 E. LINCOLN AVENUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDDLGAFDAAFFNIQAGE--AESMDPQHRLLLETVYEAVTNAGMRIQDLQGTSTAVYVGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVG-----SAKTVVG
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RAHWAY
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MCADA, PHYLLIS C.
REEVES, CHRISTOPHER D.
DAVIS, CHARLES R.
HENDRICKSON, LEE E.
RAMBOSEK, JOHN
                                                                                                                                                                                                                                            USA
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                                                                                                                                           Version
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Search completed: November 25, Job time: 1750 sec

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Best Local Similarity 23.5%;
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357
                                 327 FAGPIGYFTADNSGEFVVG 345
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                                                                                                                                        251 -VVLKTLSQALRDGDTIECVIRETGVNQDGRTTGITMPNHSAQEALIKATYAQ------
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                                                                                                                                                                                                                                      183 VLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEH
                                                                                                                                                                                                                                                                                                                                                                                    63 QSFDEQEYPQSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 QSDLQQLYAALETTEFGAYFATPADDTLRFGIGAIATAKT-----AQALQG---AVF-GA 62
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                                                                    ----AGLDITKAEDRCQFFEAHGTGTPAGDPQEAEA--IATAFFGHEQVARSDGNERAPL
                                                                                                                                                                                                                                                                                                                      HVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANTYHV 182
                                                                                                                                                                                                              -----LILGPMTFVLES--KLSMLSPSGRSRMWDAGADGYARGEAVCS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89;
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366
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Title:
Perfect score:
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ALIGNMENTS

A;Accession: S27507 A;Molecule type: DNA A;Residues: 1-11,'K',13-110,'WDLCYSEDFLITLAKKEVHNGTISRKGISLCLRLC' <row1> A;Cross-references: EMBL:M74538; NID:g1185287 A;Cross-references: DNA A;Accession: S27508 A;Molecule type: DNA A;Residues: 151-471 <row2> A;Cross-references: EMBL:M74538; NID:g1185287 A;Cross-references: EMBL:M74538; NID:g1185287 A;Cross-references: EMBL:M74538; NID:g1185287 A;Miller, P. J. Bacteriol. 170, 2742-2748, 1988 A;Title: Transcriptional regulation of a promoter in the men gene cluster of Bacillus A;Reference number: 139883; MUID:88227858 A;Reference number: 139883; MUID:88227858 A;Accession: 139883 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-11,'K',13-32 <mil> A;Cross-references: GB:M21320; NID:g143178; PIDN:AAA22594.1; PID:g551715 R;Driscoll, J.R.; Taber, H.W.</mil></row2></row1>	probable isochorismate synthase (EC 5.4.99.6) menaquinone-specific menF - Bacillus subtilis C;Species: Bacillus subtilis C;Bacies: Bacillus subtilis R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Rature 390, 249-256, 1997 A;Authors: Toulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masudaj S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Korcha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se Rekuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya A;Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A;Recession: A69507 A;Exerimental source: strain 168 R;Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H. B;Rowland, B.; Hill, K.; Mueller, J.; Driscoll, J.; Taber, H. B;Reference number: S27507 A;Bereference number: S27507	

J. Bacteriol. 174, 5063-5071, 1992 A; Title: Sequence organization and regulation of the Bacillus subtilis menBE operon.

387

399

327 339 267 279

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A; Molecule type: DNA
A; Residues: 151-471 <DR2>
A; Cross-references: EMBL:M74521;
C; Genetics:
                                                                                                                                                                                                                                   pchA protein - Pseudomonas aeruginosa C;Specias: Pseudomonas aeruginosa C;Specias: Pseudomonas aeruginosa C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: $60203; SS8229 R;Serino, L.; Reimmann, C.; Baur, H.; Beyeler, M.; Visca, P.; Haas, D. Mol. Gen. Genet. 249, 217-228, 1995 A;Title: Structural genes for salicylate biosynthesis from chorismate in Pseu A;Reference number: $60202; MUID:96086939 A;Accession: $60203
                                                                                                                 A;Cross-references: EMBL:x82644; NID:g1628425; PIDN:CAA57969.1; A;Note: this protein is involved in salicylate biosynthesis C;Superfamily: isochorismate synthase
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C;Superfamily: isochorismate synthase
C;Keywords: intramolecular transferase;
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A;Molecule type: DNA
A;Residues: 1-11,'K',13-110,134-135,'LCYSE',141-142,'LL','T',317,'AKKEVHN',325,'T',327,
A;Cross-references: EMBL:M74521; NID:g557486; PIDN:AAA50396.1; PID:g557487
A;Accession: T46639
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A; Residues: 1-476 <SE2>
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                                    22.5%;
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Pred. No. 2.4e:
77; Mismatches
                    Score 453; DB
Pred. No. 5.2e
38; Mismatches
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.2e-27;
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A; Accession: S75568
A; Status: nucleic acid
A; Molecule type: DNA
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C;Superfamil
C;Keywords:
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A;Cross-references: EMBL:D90911; GB:AB001339;
A;Note: the nucleotide sequence was submitted
C;Genetics:
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A; Title: Sequence
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Matches 112;
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LDYGSRLNVAHCLQRLRQQYGDCYLFSWGNGQGDCFYGASPERLLSLHNQQLYTDALAGS
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                                                          HLWTQTQAPLPPHIHPLALVQQLHPTPAVAGVPVAIAEDLIRRHETFDRNLYAAPLGWLD
                                                                                               HLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFT
                                                                                                                                      APRDVDVQGDRQLGQELLHNPKELREHQAVLDYLLQRLRALGLSPQASSL-KLLKLANIQ
                                                                                                                                                                            SRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTTSLKVPAMPSLLKNKQVQ
                                                                                                                                                                                                                                                   LQLSDTLRLAQIIRALAEQANTYHVVL--KRHDELFISATPERLVAMSGGQIATAAVAGT
                                                                                                                                                                                                                                                                                              LSATRRAQPARDTHTPSMVVKAPRLTGIEVAKLSKAIASSLEEIA • QQRLSKVVLATALD
                                                                                                                                                                                                                                                                                                                                  LAQFVPKQP--NTVTTSHVTD-----EVDWIERT-ENLIDTLAIDQTLAKVVFGRQQT
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Pred. No. 1
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cyanobacterium

PID: g165

Yamada,

мiyajima, ida, м.; Ya Synechocys

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Gaps

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N;Alternate names: isochorismate synthetase
C;Species: Escherichia coli
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989
C;Datesion: JT0497; S04323; I73520; G64792
C;Accession: JT0497; S04323; I73520; G64792
R;Ozenberger, B.A.; Brickman, T.J.; McIntosh, M.A.
J. Batteriol. 171, 775-783, 1989
                                                                               A:Molecule type: DNA
A;Residues: 1-391 <0ZE>
A;Cross-references: GB:M24142; NID:g341117;
R;Elkins, M.F.; Earhart, C.F.
FEMS Microbiol. Lett. 56, 35-40, 1988
                                                                                                                                                                               A; Title: Nucleotide sequence of Escherichia coli isochorismate A; Reference number: JT0497; MUID:89123153
A; Accession: JT0497
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A;Gene: entC
C;Superfamily: isochorismate synthase
                                        R;Elkins, M.F.; Earhart, C.F.
FEMS Microbiol. Lett. 56, 35-40, 1988
A;Title: An Escherichia coli enterobactin
A;Reference number: S04323; MUID:90236256
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A;Experimental source: strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A; Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; He Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable entC protein - Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998
C;Accession: H70595
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        A;Status: preliminary
                          A; Accession:
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36.6%;
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Pred. No. 1.2e-19;
5; Mismatches 129;
                                                             cluster gene with
                                                                                                                      PID:g450376
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                                                             sequence homology
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                                                             RESULT
C69615
isochorismate synthase dhbC -
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_
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C; Keywords:
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A:Map position: 14 min
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-33 < RES>
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Best Local
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les 113; Conserv
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subtilis
#sequence_revision
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R;Brickman, T.J.; Ozenberger, B.A.; McIntosh, N. J. Mol. Biol. 212, 669-682, 1990
A;Title: Regulation of divergent transcription A;Reference number: 156426; MUID:90230305
A;Accession: 173520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000165; GB:U00096; NID:g1786808; PIDN:AAC73694.1; A;Experimental source: strain K-12, substrain MG1655 C;Comment: This enzyme catalyzes the isomerization of chorismate to isochor of the entC gene is regulated by iron and possibly by the product of the entC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-391 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G64792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: EC 5.4.99.6 (validated; MUID:89123153) A; Pathway: enterobactin biosynthesis; menaguinone bic C; Superfamily: isochorismate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X53274; NID:g48747; PIDN:CAA37371.1; R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; A.; Rose, D.J.; Mau, B.; Shao, Y.
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A; Residues: 1-304, 'TA', 307-391 <ELK>
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                                                                                                                                                                                                                                                                     LLASQKNRIEHQYVVASITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSV
                                                   NQTQRRATLFAGAGIVADSDAQQEYEETGLKFEPM
                                                                                                       LTLACLLHPTPALSGFPHQAATQVIAELEPFDRELFGGIVGWCDSEGNGEWVVTIRCAKL
                                                                                                                                                             TAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                           SQSLNVVERQAIPEQTTFEQMVARAAALTATPQVDKVVLSRLIDITTDAAIDSGVLLERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERTENLIDTLAI-DQTLAKVVFGRQQTLQLS---DTLRLAQIIRALAEQANTYHVVLKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAALETTEFGAYFATPA-----DDTLRFGIGAIATAKTAQALQGAVF-GAQSFDEQEYP
                                                                                                                                                                                                                                                                                                                              IAQNPVSYNFHVPLADGGVLLGASPELLLRKDGERFSSIPLAGSARRQPDEVLDREAGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWI 131
                                                                                                                                                                                                                    LLASEKDRHEHELVTQAMKEVLRERSSELHVPSSPQLITTPTLWHLATPFEGKANSQENA
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28.6%;
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Pred. No. 8.3e-19;
5; Mismatches 153
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384
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Bacillus

10-sep-1999 subtilis

#text_change

16-Jun-2000

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siderophore biosynthetic protein amoA - Aero C; Species: Aeromonas hydrophila C;Date: 10-Sep-1999 #sequence_revision 10-Sep C; Accession: A40365 R;Barghouthi, S.; Payne, S.M.; Arceneaux, J. J. Bacteriol. 173, 5121-5128, 1991 A;Title: Cloning, mutagenesis, and nucleotic A;Reference number: A40365; MUID:91317731 A;Accession: A40365
A; Accessic
A; Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Authors: Foolger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Reference number: A6980; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: C69615
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
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C;Superfamily: isochorismate synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-398 < KUN>
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                                                                                                                                                                                                                                                                                                                               ATLFAGAGIVADSDAQQEYEETGLKFEPM 386
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                                                                                                                                                                                                                                                                                                                                                                                                                LHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRHDE-----LFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDYKNGVEQGLARIA-DGTLSKIVLSRSLHLTSPEPIQTDELLRHLAQHNSHGYTFAADV
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                                          is, and nucleotide MUID:91317731
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Pred. No. 1.:
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                                                                                                                                                                                    Aeromonas hydrophila
                                                                                                     J.E.
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                                                             sequence of
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                                                                                                                                           #text_change
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A; Molecule type: DNA
A; Residues: 'MLLTRRE', 30-93, 'E', 95-356 <MUE>
A; Cross-references: EMBL: Z50849; NID: g1050906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-396 cBAP>
A; Cross-references: GB:M63339
A; Note: the authors translated the codon GAG
C; Superfamily: isochorismate synthase
                                                           В
                                                                                                                                                                                                                                                                                                                                                                                           A;Title: An isochorismate hydroxymutase isogene in A;Reference number: S68696; MUID:96140724 A;Accession: S68696
                   20
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                                                                                                                                                                                                                                               A;Gene: meni
C;Keywords:
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A; Residues: 1-356 <BLAT>
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                                                                                                                                           Query Match
Best Local S
Matches 106
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QFVPKQP-----NTYTTSHYTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDT 163
                                                             IWGLNAFDPSQ------GNLLLPRLEWRRCGGKATLRLTLFSESSLQHDAIQAKEFIA
                                                                                                   VFGAQSFDEQEYPQSELMAGEWEVPEVMVTIAADKITFGSDTVSDFT---
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                                                                                                                                             106;
                                                                                                                                                                                                                                               intramolecular transferase;
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                                                                                                                                           Similarity 30. 06; Conservative
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30.3%;
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                                                                                                                                             51;
                                                                                                                                       Score 317.5; |
Pred. No. 7.6e
51; Mismatches
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Pred.
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isochorismate synthase (EC 5.4.99.6) - Escherichia coli
C;Speciaes: Escherichia coli
C;Speciaes: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C;Accession: G64997; S68696; S61203
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000316; GB:U00096; NID:g1788594; PIDN:AAC75325.1; PID:g17886
A;Experimental source: strain K-12; substrain MG1655
R;Mueller, R; Dahm, C; Schulte, G;; Leistner, E.
FEBS Lett. 378, 131-134, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 LAKVVFGRQQTLQLSDTLRLAQII-RALAEQANTYHVVLK-RHDELFISATPERLVAMSG 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RALFSGIVGWCDSQGNGEWAVVIRCGVLDGHQ--VELFAGAGIVAGSDPPWSGPRPGTKL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation
                                                                                                                                                                                                                                                                                                     PID:g1050907
                                                                                                         DB 2;
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anthranilate synthase (EC 4.1.3.27) component I [validated] - Sulf
N.Alternate names: anthranilate synthase alpha chain
C;Species: Sulfolous solifataricus
C;Date: 15-May-1997 #sequence_revision 18-Jul-1997 #text_change 17
C;Accession: JC5323; A40635
R;Tutino, M.L.; Tosco, A.; Marino, G.; Sannia, G.
Biochem. Biophys. Res. Commun. 230, 306-310, 1997
A;Title: Expression of Sulfolobus solifataricus trpE and trpG genes
A;Reference number: JC5323; MUID:97168965
A;Accession: JC5323; MUID:97168965
A;Accession: JC5323; MUID:97168965
A;Accession: JC5323
A;Status: nucleic acid sequence not shown
A;Reference number: DNA
A;Residues: 1-421 < TUT>
R;Tutino, M.L.; Scarano, G.; Marino, G.; Sannia, G.; Cubellis, M.V
J. Bacteriol. 175, 299-302, 1993
A;Title: Tryptophan biosynthesis genes trpEGC in the thermoacidoph
A;Reference number: A40635; MUID:93106970
A;Accession: A40635
A;Status: preliminary
A;Accession: A40635
A;Cross-references: GB:M98048; NID:93106970
A;Cross-references: GB:M98048; NID:93106970
A;Residues: 1-421 < TUZ>
A;Cross-reference extracted from NCBI backbone (NCBIN:121234, NCBIF
C;Genetics:
A;Gene: trpE
C;Complex: heterotetramer; two component I chains (PIR:JC5323), tw
C;Function: CANT>
A;Description: EC 4.1.3.27 [validated; MUID:9380543]
A;Note: magnesium required
C;Superfamily: anthranilate synthase component I
C;Reywords: carbon-carbon lyase; oxo-acid-lyase; tryptophan biosynthase;
C;Genetianily: anthranilate synthase component I
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                                                                                                                                                                                                Local Similarity
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                                                                                                                                                DDTLRFGIGAIATAKTAQ---ALQGAVFGAQSFD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNAAAMMAASRRLNLNCYHFYMAFDGENAFLGSSPERLWRRRDKALRTEALAGTVANNPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRLAQIIRALAE-QANTYHVVLKRHDE-LFISATPERLVAMSGGQIATAAVAGTSRRGTD
    DWIERTENLIDTLAIDQTLAKVVFGR-QQTLQLSDTLRLAQIIRALAEQANTYHVVLKRH
                                                                                                                  DDPVNILNGYLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCVSLRSAKISGNVVR--LYAGAGIVRGSDPEQEWQEIDNKAAGLRTLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLVSIKPLPGLHLTTTREQHWPDKTGWTQLIELATKTIA-EGELDKVVLARATDLHFASP
                                                    -FFTPDNIIIYDHNEGKVYVNADLSSVGG--CGDIGEFKVSFYDESLNKNSYERIVSESL
                                                                                                                                                                               Conservative
                                                                                 EVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDE-V
                                                                                                                                                                                              14.4%;
24.9%;
                                                                                                                                                                          72;
                                                                                                                                                                            Score 289; DB 2;
Pred. No. 1.5e-14;
2; Mismatches 163
                                                                                                                                                                                                                                                                                                                                                                                                      chains (PIR:JC5323),
                                                                                                                                                                             163;
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NCBIP:121235)
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RESULT
A42301
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Best Local S
Matches 79
                                                                                                                                                                               471
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anthranilate synthase (EC 4.1.3.27) alpha chain - Haloferax volcanii C;Species: Haloferax volcanii C;Date: 10-Jul-1992 #sequence_revision 18-Sep-1992 #text_change 22-J C;Accession: A42301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M83788; NID:g149036; PIDN:ANA73177.1;
A;NOte: the authors failed to give the translation for ACC in
C;Superfamily: anthranilate synthase component I
C;Keywords: carbon-carbon lyase; oxo-acid-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lam, W.L.; Logan, S.M.; Doolittle, W.F. J. Bacteriol. 174, 1694-1697, 1992 A;Title: Genes for tryptophan biosynthesis A;Reference number: A42301; MUID:92165748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-523 <LAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TTSHVTDEVDW---IERTENL---IDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRAL
                                                                                               FDATRATFPAGTLTGAPKVRAMEIIDDLEAEPRGVYGGGVGYYSWTGDADVAIVIRTATV
                                                                                                                                                                                                                                                                                                  --NPSPYMFLLRHGDRRVVGASPETLVSVRGDRVVVNPIAGTCQRGSGPVEDRRLAGELL
                                                                                                                                                                                                                                                                                                                                                                                                            TKEHVRDGDIYQGVISRTRKLRGQVDPVGLYASLREV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVADSDAQQEYEETGLKFEPMR 387
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DSGGADDAITVRAGAGIVADSDPTAEYEETEQK
                                          NQ--TQRRATLFAGAGIVADSDAQQEYEETGLK
                                                                                                                                               TAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYV
                                                                                                                                                                                                                                                    ASQKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSV
                                                                                                                                                                                                                                                                                                                                                       AEQANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DELFISATPERLYAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVA
                                                                                                                                                                                                  ADAKERAEHTMLVDLGRNDVRRVSTPGSVRVEDFMSIIKYSHVQHIESTVSGTLDADADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 278.5; DB 2;
Pred. No. 1.3e-13;
4; Mismatches 115;
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n residue 239
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Kerlavage 1.; Weidman jen, N.S.M.

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A;Gene: trpE
C;Superfamily
C;Keywords: c
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A;Residues: 1-456 <BAR>
A;Cross references: EMBL:M87483; NID:g149514; PIDN:AAA25223.1; PID:g149516
C;Genetics:
                                                                                                                                                                                                                                                                                                                    anthranilate synthase (EC 4.1.3.27) alpha chain - Lactococcus lactis subsp. C:Species: Lactococcus lactis subsp. lactis C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999 C:Accession: S35124 R:Bardowski, J.; Ehrlich, S.D.; Chopin, A. J. Bacteriol. 174, 6563-6570, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
S35124
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C;Superfamily: isochorismate synthase
C;Keywords: intramolecular transferase; isomerase
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                                                                                                                                                                                                                                                                   A;Title: Tryptophan biosynthesis genes in A;Reference number: S35123; MUID:93015708 A;Accession: S35124
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A; Residues: 1-430 <TIGR>
A; CC: C: C: GB: U32714; GB: L42023; C: Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae IA;Reference number: A64000; MCID:95350630
A;Accession: E64059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown; translation not
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Best Loc
Matches
                                                                                                                          Superfamily: anthranilate synthase component I;
Keywords: carbon-carbon lyase; oxo-acid-lyase; tryptophan biosynthesis
                                                         Query Match
Best Local Similarity
                                       Matches
 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412
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Local Similarity
KVVFGRQQTLQLSDT-----LRLAQIIRALAEQANTYHVVLKRHDELFISATPERLVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRATLFAGAGIVADSDAQQE 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVESFDVSNV-ELKPLRKVQHLIRKIRANLTAHYADVNILKAIHPTAAVSGLPQQQAKMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTTSLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQALQGAVFGAQSFDE----QEYPQSE---LMAGFWF------VPEVMV------TIAA 91
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                                   13.6%;
llarity 29.6%;
Conservative 4
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                                   ; Score 272.5; DB 2; 
pred. No. 3e-13; 
49; Mismatches 101;
                                                                                                                                                                                                                                                                                                        Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:g1573241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 2; Length 430;
le-13;
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                                     Indels
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                                                                         Length
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                                                                                                                                                                                                                                                                                                      subsp. lactis
                                     19;
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 201
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RESULT

probable anthranilate synthase component I C; Species: Streptomyces coelicolor

Streptomyces

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Garnier, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holing Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987

A;Accession: G70556

A;Accession: G70556
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C; Superfamily:
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C; Species: Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z95554; GB:AL123456; NID:g3261771; PIDN:CAB08903.1; PID:g32617 A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-516 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 EVMVTIAADKITFG-----SDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWIER 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
AYVQAGGGVVADSNGSYEYNE
                                         LF--AGAGIVADSDAQQEYEE 378
                                                                                                                                                                                                                                                  NSDGAVDFSIVGSSPEALVTVHEGWATTHPIAGTRWRGRTDDEDVLLEKELLADDKERAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHGNQVSTNPIAGTRKRGQTEFEDQALIEDLESDPKEVAEHKMLVDLGRNDIGKISKYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAGTLSGAPKVRAMELIEEVEKTRRGLYGGVVGYLDFAGNADFAIAIRTALM-,---RNGT 467
                                                                                                                       PTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRAT 359
                                                                                                                                                                    HLMLVDLGRNDLGRVCTPGTVRVEDYSHIERYSHVMHLVSTVTGKLGEGRTALDAVTACF 411
                                                                                                                                                                                                       HQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLH 299
                                                                                                                                                                                                                                                                            RHDEL----FISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIE 241
                                                                                                                                                                                                                                                                                                                                     TVEEYGAIVEYLVDQIAAGEAFQVVPSQRFEMDTDVDPIDVYRILRVTNPSPYMYLLQVP 291
                                                                                                                                                                                                                                                                                                                                                                         T-----ENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANTYHVVLK 185
                                                                                                                                                                                                                                                                                                                                                                                                                     EGTITLIANAVNWNGTDERVDWAYDDAVARLDVMTAALGOPLPSTVATFSRPEPRHRAOR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRATLFAGAGIVADSDAQQEYEET 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEVPVFMKVEKYRYVMHITSEVTGELRPEFTAMDALRATLPAGTLSGAPKHRAYQRIYEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 257;
Pred. No. 5.
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5.5e-12;
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Holroyd,
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geno

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anthranilate synthase component I [imported] - Pyrococcus kodakaraensis C;Species: Pyrococcus kodakaraensis C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000 C;Accession: T43924 R;Imanaka, T.; Ezaki, S.; Atomi, H. submitted to the EMBL Data Library, July 1999 A;Description: Trp operon of Pyrococcus kodakaraensis KOD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000 C;Accession: T36306
R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
A;Accession: T36306
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                                                                                                    В
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C;Superfamily: anthranilate synthase component I
                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AB030011; PIDN:BAA82547.1 A;Experimental source: strain KOD1
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-433 <IMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z22725
A; Accession: T43924
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C;Superfamily: anthranilate synthase component I
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       В
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Best Local S
Matches 83
                                                                                                                                                                                                 Query Match 12.6%; Score 252.5; DB 2; Best Local Similarity 27.8%; Pred. No. 9.4e-12; Matches 68; Conservative 56; Mismatches 112;
352 NQTQRRATLFAGAGIVADSDAQQEYEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 QANTYHVVL--KRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TSHVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLR-----LAQIIRALAE 175
                                                                                                      190
                                                                                                                          468 -- ADGHVHVQAGAGIVADSDPAAEFRET 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 LDALRSAFPAGTLSGAPKIRAMEITAELEPEQRGVYGGALGFVGADGLTDFATALRTMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 TAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 ADEKERAEHVMLVDLGRNDLGRVTEPGTVRVERLMRVERFSHVMHLSSTVRGRLAEGRDA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 ASQKNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 SPYMYHLSLGGGRH----VIGASPELLVKAEGRTVRTRPLAGTRPRHPDPAEDLRLERELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 TANLT-EAQFTERVARAREHIAAGDAF-QIVLSR----RLSRPLRARPTDLYRHLRATNP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 83; Conserv
                                                                                               QVVLSREYRVRTD--LDALEIYKRLVELNPSPYTFILEFEKTVVGASPETMGSVEGRTFK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 253; DB 2; Length 511; 31.0%; Pred. No. 1.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                              Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 124; Indels
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                                                                                                                                                                                                                                           Length 433;
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                                                                                                308 DVLKYSHVQHIESEVVGELDEGKNAFDAMEAAFPAGTLTGAPKIRAMEIIDELERSRRKV 367
                                                                                                                         267
RAVLK 427
                                                 YGGAVGYFSLTGDADMAIAIRMAEIE--GRKASVRAGAGIVADSVPEKEFFETENK---M 422
                                                              SLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGL 326
                         RQLLK 391
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Search completed: November 25, 2000, 02:18:56 Job time: 1383 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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                               Serino L., Reimmann C., Baur H., Beyeler "Structural genes for salicylate biosynt) Pseudomonas aeruginosa.";
Mol. Gen. Genet. 249:217-228(1995).
-I- FUNCTION: INVOLVED IN THE CONVERSION
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01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
SALICYLATE BIOSYNTHESIS ISOCHORISMATE
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SEQUENCE 471 AA; 52811 MW; 94C047C549FC4CF9
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BL; ARC00220; AAC00223.1; -.
BL; M74521; AAA50396.1; ALT_SEQ.
BL; M74521; AAA50397.1; ALT_SEQ.
BL; M74521; AAA50397.1; ALT_SEQ.
BL; M21320; AAA22594.1; -.
BL; M21320; CAB15061.1; -.
R; S27508; S27508.
 CATALYTIC PATHWAY: S
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PF00425; chorismate_bind;
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STRAIN-K12;
MEDLINE; 90236256.
Elkins M.F., Earhart C.
"Opacity factor from gr
"Opacity factor Lett. 5
                                                                                                                                                                                                                                   ENTC_ECOLI
P10377;
01-MAR-1989
01-OCT-1994
01-NOV-1997
                                                                                                                                                                                                                                                                                      _ECOLI
                 Ozenberger B.A., Brickman T.J., McIntosh M.A.;
"Nucleotide sequence of Escherichia coli isochorismate sy
gene entc and evolutionary relationship of isochorismate
and other chorismate-utilizing enzymes.";
J. Bacteriol. 171:775-783(1989).
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1. 35, Last annotation up
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group A streptococci
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Liu J., (
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobactin biosynthesis; Iron CONFLICT 305 306 SG SEQUENCE 391 AA; 42931 MW; 6
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INDUCTION: EXPRESSED UNDER CONDITIONS OF IRON STARVATION.
SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES; WEL
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                                                                                                                                                                                                                                                                                      Isomerase.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Duplicate isochorismate synth regulation and involvement in 2,3-dihydroxybenzoate.";
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                                                                                                                                                                                                               87; Conserv
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STRAIN-KI2 / MC4100;
MEDLINE; 96140724.
Mueller R., Dahm C., ;
"An isochorismate hydi
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STRAIN-K12 / MG1655;
MEDLINE; 97426617.
Blattner F.R., Plunke
Popp J.L.;
"Sequence
                                         SEQUENCE;
                                                                                                                                                                                                                               Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y. Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (
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pp 38051; Q47009; Q47704; p76479;
01-OCT-1994 (Rel. 30, Created)
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Riley M., Collado-Vides
Gregor J., Davis N.W., F
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MEDLINE; 96291661.
Daruwala R., Kwon O.,
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STRAIN-K12 / 1
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Bacteria; Proteobacteria;
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  menD
                                                                                                                                                                                                                                                                             H., Motomura K., Nakamura Y.,
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  gene
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    from
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RESULT 7
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ID VIBC_V
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DT 15-DEC
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Best Local Similarity
  VIBC_VIBCH
007898;
15-DEC-1998
15-DEC-1998
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: CHORISMATE = ISOCHORISMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Menaquinone biosynthesis; Isomerase.
CONFLICT 310 312 VLR -> YC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR000350; -.
PFAM; PF00425; chorismate_bind; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECOGENE; EG12362; MENF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 171:4349-4354(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L; Z50849; CAA90702.1; ... U54790; AAC44303.1; ... L; AE000316; AAC75325.1; ALT_INIT. L; D90857; CAB22015.1; ... D90858; CAB22025.1; ... L; U58768; AAB02729.1; ... L; M21787; ... NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRPE AND PABB.
CAUTION: REF.7 SEQUENCE DIFFERS FROM THAT
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SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMESHIFTS.
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                                                                                                                                                                                                                                                                FVVGIRSMYVNQTQRRATLFAGAGIVADSDAQQEYEETGLKFEPMRQLLK
                                                                                                                                                                                                                                                                                                                                                                         TGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGE
                                                                                                                                                                                                                                                                                                                                                                                                                              DKQAQQLGEWLMADDKNQRENMLVVEDICQRLQADTQTLDV-LPPQVLRLRKVQHLRRCI
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                                                                                                                                                                                                                FCVSLRSAKISGNVVR--LYAGAGIVRGSDPEQEWQEIDNKAAGLRTLLQ
                                                                                                                                                                                                                                                                                                                          WTSLNKADDVICL-HQLQPTAAVAGLPRDLARQFIARHEPFTREWYAGSAGYLSLQQS-E
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                                                                                   STANDARD;
  37, Creat
37, Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
  sequence
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Pred. No. 2.7e-16;
1; Mismatches 162;
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D081724F3329FE47 CRC64;
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  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 179:7055-7062(1997).

- CAPALYTIC ACTIVITY: CHORISMATE.
- FATHMAY: VIBRIOBACTIN BIOSYNTHESIS. VIBRIOBACTIN
CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON
BACTERIAL ENVIRONMENT INTO THE CELL CYTOPLASM.
- SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYNTHATRPE AND PABB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDITARE: 98037504.

Wyckoff E.E., Stoebner J.A., Reed K.E., Payne S.M.;

"Cloning of a Vibrio cholerae vibriobactin gene cluster:

"Cloning of a Vibrio cholerae required for early steps in side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00425; chorismate_bind;
Iron transport; Isomerase.
SEQUENCE 395 AA; 43594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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STRAIN=EL TOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U52150; AAC45925.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRPE AND PABB.
-i- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification of genes required for
biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIBRIOBACTIN-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPRO00350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel.
357
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                 AGAGIVADSDAQQEYEETGLKFE
                                                         PAVCGFPRESAYQAIRELEEFDRGYFTGMVGWCDARGNGEWVVTIRCAEVGSHQMK--LF
                                                                                                                                   QYVVASITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITGDIA-AHLSVTAIVDRLHPT
                                                                                      PALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRATLF
                                                                                                                     GLYVEEVERIMSRYCRNLYTPMYPSVIETETMLHLSTLLEGQVSDPEVCALQVAADLHPT
                                                                                                                                                                                                                                             PSGEQYKQGVSHLLNMFHHSGLSKVVLSRAIEIATEQEIALPTLLRSLLAINHHGYTFAA
AGAGIVDESLPQSELEETGAKMK
                                                                                                                                                                                  SLDEQRKL-IGASPELLVAKRGNYLISNPLAGSRPRSQDAQENAQRRASLLNTAKDLHEH
                                                                                                                                                                                                               VLKRHDELFISATPERLYAMSGGQIATAAYAGTSRRGTDGADDIALGEALLASQKNRIEH
                                                                                                                                                                                                                                                                                                                                       FVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWIERTENLIDT 14
                                                                                                                                                                                                                                                                                                                                                                      FFASANQSMLGCGVAHAFQQAIPFAELANQAKQLLQQA----KRDECDNP---LLFGI-'78
                                                                                                                                                                                                                                                                                                                                                                                                                                     109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                         -----VPFDPKTPTRFMIPRTLYVSSSPRLNRPAHLTRQV-----AKLISS
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isomerase.
AA; 43594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOU15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,
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28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
ISOCHORISMATE SYNTHASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO OTHER ISOCHORISMATE SYNTHASES; WEAK,
                                                                                                                                                                                                                                                                          -TLAKVVFGRQQTLQLSDTLRLAQIIR---ALAEQANTYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 308.5; DE Pred. No. 1.1e-17; Mismatches 1
379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2FFAF87DD948C78B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   158;
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RESULT 8
TRPE_SULSO

TRPE_SULSO

STANDARD;

PRT;

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A Knoechel T., Ivens A., Hester G., GUITAMINE STRUTTY: CHORDNENTS I AND TWO COMPONENTS II.

CC -!- CATHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

CC -!- SUBUNIT: TETRAMER OF TWO COMPONENTS II.

CC -I- SUBUNIT: TETRAMER OF TWO COMPONENTS II.

CC GUITAMINE AMIDOTRANSFERASE ACTIVITY. WHEREAS COMPONENT II PROVI

CC GUITAMINE AMIDOTRANSFERASE ACTIVITY.

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01-FEB-1994
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                                                                                                                                                                                                 Tryptophan SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-ATCC 49255 / MT4;

Tutino M.L., Cubellis M., Sannia G., Marino G.;

"The tryptophan operon in Sulfolobus solfataricus.";

Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                       EMBL;
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A40635; A40635.
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                                                                                                            DDTLRFGIGAIATAKTAQ---ALQGAVFGAQSFD------EQEYPQSELMAG
                                     -FFTPDNIIIYDHNEGKVYVNADLSSVGG--CGDIGEFKVSFYDESLNKNSYERIVSESL
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95; Conser
                                                                                                                                                                                                                                                                                                                      and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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72; Mismatches
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"Genes for tryptophan biosynthesis in the halophilic archaebacterium Haloferax volcanii: the tryDFEG cluster.";

J. Bacteriol. 174:1694-1697(1992).

-!- CATALTTC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTHRANILATE + PYRUVATE + L-GLUTAMATE.

-!- PARHWAY: FIRST STEP IN BIOSYNTHESIS OF TRYPTOPHAN.

-!- SUBUNIT: TETRAMER OF TWO COMPONENTS I AND TWO COMPONENTS II (BY
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long a
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SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTH
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                                        TTSHVTDEVDW---IERTENL---IDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRAL
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
MENAQUINONE-SPECIFIC ISOCHORISMATE SYNTHASE (MENE OR HI0285.
                                                                                                                  TIGR; HIO:
INTERPRO;
                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
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Bacteria; Proteobacteria;
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Menaquinone biosynthesis; Isomeras
SEQUENCE 430 AA; 48466 MW; 3BP
                                                                                                                                                                        entities
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SIMILARITY: STRONG, TO OTHER ISOCHORISMATE SYN
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HI0285; -.
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                                 Conservative
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27
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MW; 3BA1:
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Pred.
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                                 Mismatches
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                      Tryptophan biosynthesis; Lyase.
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TRPE_LACLA
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01-APR-1993
30-MAY-2000
                                              modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                 EMBL;
                                                                                                                                                        This
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"Tryptophan biosynthesis genes in Lactococcus lacti
J. Bacteriol. 174:6563-6570(1992).
-i- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE -
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PATHWAY: FIRST STEP IN B:
SUBUNIT: TETRAMER OF TWO
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es; Bacillus/Clostridium group;
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"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ANTHRANILATE SYNTHASE COMPONENT I (EC 4.1.3.2
TRPE OR RV1609 OR MTCY01B2.01 OR MTV046.07.
                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                         EMBL; 295554; CAB08903.1; TUBERCULIST; RV1609; -.
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SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTH
                                                                                                                                                                                                                                                                                                        PYRUVATE + L-GLUTAMATE.

PATHWAY: FIRST STEP IN BIOSYNTHESIS SUBURIT: TETRAMER OF TWO COMPONENTS
                                                                                                                                                 European Bioinformatics Institute.
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                                                                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                            COMPONENT
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                           EMBL; ALO:
INTERPRO;
                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRPE OR SCE8.07C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases -- -- CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE - ANTH
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PATHWAY: FIRST STEP IN BIOSYNTHESIS SUBUNIT: TETRAMER OF TWO COMPONENTS
                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: COMPONENT I CATALYZES USING AMMONIA RATHER THAN GLUTAMINE, GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
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                           AL035654; CAB38585.1; PRO; IPR000350; -.
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
E SYNTHASE COMPONENT I (EC 4.1.3.27).
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Tang X., Ezaki S., Fujiwara S.,
"The tryptophan biosynthesis gen
kodakaraensis KOD1 is regulated
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                                                  or send an
                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                           STRAIN-KOD
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTHRANILATE
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              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRPE_PYRKO
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                                                                                                                                                            MISCELLANEOUS: COMPONENT I CATALYZES THE FORM USING AMMONIA RATHER THAN GLUTAMINE, WHEREAS GLUTAMINE AMIDOTRANSFERASE ACTIVITY. SIMILARITY: BELONGS TO THE ANTHRANILATE SYNTH
                                                                                                                                                                                                                         PYRUVATE + L-GLUTAMATE.

PATHWAY: FIRST STEP IN BIOSYNTHESIS SUBUNIT: TETRAMER OF TWO COMPONENTS
                                                                                                                                                                                                                                                                 . Gen. Genet. 262:815-821(1999).
CATALYTIC ACTIVITY: CHORISMATE + L-GLUTAMINE =
                                                                                                                                                                                                                  SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ADGHVHVQAGAGIVADSDPAAEFRET
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                         AB030011; BAA82547.1;
  PF00425;
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                                               and this statement is not removed requires a license agreement (See an email to license@isb-sib.ch).
                                                                                    non-profit institutions as long
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             IPR000350;
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31.0%;
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Last annotation update)
COMPONENT I (EC 4.1.3.27).
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s gene cluster trpCDEGFBA fi
ated at the transcriptional
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Pred. No. 1
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                                                           (See http://www.isb-sib.ch/announce/
                                                                                  There are no rest
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..9e-11;
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                                                                                                                                                             SYNTHASE COMPONENT
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                                                                       Usage
                                                                                                                                                                                                    FORMATION OF ANTHRANILATE
                                                                                                                                                                                                                           TWO COMPONENTS
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from Pyroco
                                                                                               restrictions
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Best Local Similarity
Matches 68; Conser
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01-DEC-1992
01-DEC-1992
                                                                                                                    SUBTILLARITY: BELONGS TO THE ANTHRANILATE SYNTHASE COMPONENT I
                                                                                                                                                                                                                                                                                                                                      Ogasawara N., Nakai S., Yoshikawa H.;
Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the
"Systematic sequencing of the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Slock J., Stahly D.P., Han C.-Y., Six E.W., Crawford I.P.; "An apparent Bacillus subtilis folic acid biosynthetic operon containing pab, an amphibolic trpG gene, a third gene required for synthesis of para-aminobenzoic acid, and the dihydropteroate synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00095; ANTSNTHASEI.
Tryptophan biosynthesis; Lyase.
SEQUENCE 433 AA; 48541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
MEDLINE; 96051385.
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us group; Bacillus.
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ismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M34053; AAA22694.1; -.
EMBL; D26185; BAA05309.1; -.
EMBL; Z99104; CAB11850.1; -.
PIR; A37854; A37854.
SUBTILIST; BG10137; PABB.
INTERPRO; IPR000350; -.
PFAM; PF00425; ChOrismate_bind; 1.
PRINTS; PR00095; ANTSWITHASEI.
Lyase; Folate biosynthesis.
SEQUENCE 470 AA; 53251 MM; CA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                       QRRATLFAGAGIVADSDAQQEYEETGLKFEPMRQLLK 391
                                                                                                                                                                                                  KERAEHVMLVDLERNDLGRVSRYGSVRVNEFMAIEKYSHVMHIVSNVQGELQDGYDAVDI 366
                                                                                                                                                                                                                        KNRIEHQYVVASITTRLQDVTT--SLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAI 294
                                                                                                                                                                                                                                                                                             ANTYHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQ 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAQS--RKHHVLLESARGGRYSIA------GLDPIATVKGKDGITTIKHGDEMLFKEG 74
                                                                                                                                  IHAVFPGGTITGAPKVRTMEIIEELEPTRRGLYTGSIGWFGYNHDLQFNIVIRTIYA--T 424
                                                                                                                                                                    VDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQT 354
                                                                                                                                                                                                                                                                                                                                          SFAAPFTED-----GFSQAVEKIKQYIASGDVFQVNLSIRQSQSLSVHPYQIYKTLREVN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                AADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTD-EVDWIER------- 133
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Search completed: November Job time: 718 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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1: sp_archea:*
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2009
1 MATYHETRALAQSDLQQLYA.....ETGLKFEPMRQLLKDYNHVE 397
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sp_rodent:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	No.	7
214.5	215	215.5	216	216.5	217.5	218.5	219	227	251.5	295.5	304.5	307.5	307.5	344	354.5	360	383	1998.5	Score	
10.7	10.7	10.7	10.8	10.8	10.8	10.9	10.9	11.3	12.5	14.7	15.2	15.3	15.3	17.1	17.6	17.9	19.1	99.5	Match Length	*
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Q9rth3 deinococcus	Q9rqg2 rhodobacter			Q9z396 yersinia pe	Q9x9i8 yersinia en	094582 schizosacch	P72539 streptomyce		Q9vlg5 pyrococcus	Q9tm09 cyanidium c	P95475 pseudomonas	Q9s7h8 arabidopsis	O81522 arabidopsis	P77099 escherichia	005851 mycobacteri	Q9zpc0 catharanthu	P74053 synechocyst	Q9uia3 homo sapien	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
113	124	129	131	131	131.5	131.5	132	149	150	151	153	161.5	167	171	177.5	181.5	187.5	187.5	189.5	195	199.5	199.5	202.5	202.5	210.5
5.6	6.2	•	•			6.5	•									9.0				9.7	•	•	•	10.1	10.5
824	623	336	336	336	336	336	348	559	458	328	567	718	518	391	917	577	979	669	606	616	608	450	613	522	364
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Q9Y7F1	030589	Q46683	Q57446	Q57139	Q46682	Q46681	067217	025066	005591	Q57527	Q9ZME2	094277	Q9R5Z6	Q9RMT7	Q9ZV26	Q9XJ30	Q9Y1K0	Q56151	Q9xJ29	081533	Q41155	P71758	Q41156	Q9RQ44	P78905
	_	Q46683 escherichia		Q57139 escherichia	Q46682 escherichia	Q46681 escherichia	067217 aquifex aeo			Q57527 haemophilus	Q9zme2 helicobacte	094277 schizosacch		Q9rmt7 streptomyce	Q9zv26 arabidopsis	Q9xj30 oryza sativ	Q9y1k0 plasmodium	m	Q9xj29 oryza sativ	O81533 nicotiana t	Q41155 ruta graveo	P71758 mycobacteri	Ċ	Q9rq44, buchnera ap	P78905 schizosacch

ALIGNMENTS

Qy	DP QA	Ф	ру	3.00	RESULT Q9UIA3 ID Q ACC DT OO DT OO DT OO OCC RRN OCC RRN OCC RRD OCC R
180 YHVVLKRHDELFISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNR 239	120 TTSHVTDEVDWIERTENLIDTLAIDQTLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANT 179 	60 FGAQSFDEQEYPOSELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQDNTV 119 	1 MMTYHETRALAQSDLQQLYAALETTEFGAYFATPADDTLRFGIGAIATAKTAQALQGA-V 59 	Query Match 99.5%; Score 1998.5; DB 4; Length 398; Best Local Similarity 99.7%; Pred. No. 1.6e-146; Matches 397; Conservative 0; Mismatches 0; Indels 1; Gaps	JULT 1 JOHAN 2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 14, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) NEUTRAL SPHINGOMYELINASE. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1] SEQUENCE FROM N.A. TISSUS-KIDNEY; Chatterjee S., Han H., Rollins S., Cleveland T.; "Molecular cloning, Characterization, and expression of a novel human neutral sphingomyelinase."; J. Biol. Chem. 274:37407-37412(1999). EMBL; AF069740; AAF19052.1; INTERPRO; JPR000350; PFAM; PF00425; Chorismate_bind; 1. PRINTS; PR00095; ANTSWTHASEI. SEQUENCE 398 AA; 43590 MW; 0248D89974C77BC1 CRC64;

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Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL: D90911; BAA18129.1; -.
INTERPRO; IPROBOTION -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPRO00350; -.
PFAM; PF00425; chorismate_bind;
PRODOM; PD000779; -; 1.
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Naka Kaneko T., Sato S., Kimura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yamada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel.
01-FEB-1997 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
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                                 ADNSGEFVVGIRSMYVNQTQRRATLFAGAGTVADSDAQQEVEETGLKFEPM-RQLL
                                                                                                                           HLYTPITGDIAAHLSVTAIVDRLHPTPALGGVPREAALYYIATHEKTPRGLFAGPIGYFT
                                                                                                                                                                                                                   SRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTTSLKVPAMPSLLKNKQVQ
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                                                                                                 HLWTQIQAPLPPHIHPLALVQQLHPTPAVAGVPVAIAEDLIRRHETFDRNLYAAPLGWLD
                                                                                                                                                                                             APRDVDVQGDRQLGQELLHNPKELREHQAVLDYLLQRLRALGLSPQASSL-KLLKLANIQ
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Pred. No. 1.2e-21;
6; Mismatches 150
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Best Local S
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                                                               005851;
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01-JUL-1997
01-JUL-1997
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01-MAY-1999
01-MAY-1999
ENTC.
ENTC OR RV3215 OR MTCY07D1
Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Gentianales;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
ISOCHORISMATE SYNTHASE (EC 5.4.99.6)
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EMBL; AJ006065; CAA06837.1; -.
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01-FEB-1997
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Gordon S.V., Eiglmeier K., Gas S., Barry C.E., III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hol
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Suls
Taylor K., Whitehead S., Barrell B.G.;
                                                                                                Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M. Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U82598; AABA0793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
EMBL; 295120; CAB063001.1; -.
TUBERCULIST; Rv3215; -.
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Cole S.T., Brosch
INTERPRO; IPRO00350;

PFAM; PF00425; chorismate_bind;

PRODOM; PD000779; -; 1

SEQUENCE 395 AA; 43422 MW; 4
                                                                                                                                                                                                            SEQUENCE FROM N.A. Chung E., Allen E.,
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Corynebacterineae; Mycobacteriaceae; Mycobacterium
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Pred. No. 1.3e-19;
47D925F1953DB933 CRC64;
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[7]
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                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                   INTERPRO; IPR000350; -.
PROM; PF00425; chorismate_bind;
PRODOM; PD000779; -; 1.
                                                                                                                                                                                                                                       Submitted (JUL-1998) to the EMBL; AF078080; AAC97926.1;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                             Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                            ISOCHORISMATE SYNTHASE.
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             134
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TENLIDTL-AIDQTLAKVVFGRQQTLQLSDT-----LRLAQIIRALAEQANTYHVVLKRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \tt YRSFTTSGCFARFDEPAVNGDSPDSPFQQKLAALFADAKAQGIKNPVMVGAIPFDPRQ-P
                                                                                                       ALETTEFGA-YFATPADDTLRFGIGAIATAKTA-----QALQGAVFGAQSFDEQEYPQS
                                                                                AVEWEPFGAFYFSVPQVEFNEFGGSSMLAATIAWDDELSWTLENAIEALQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTLACLLHPTPALSGFPHQAATQVIAELEPFDRELFGGIVGWCDSEGNGEWVVTIRCAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAALETTEFGAYFATPA-----DDTLRFGIGAIATAKTAQALQGAVF-GAQSFDEQEYP
                                                          ELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWIER 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RENOVR -- LFAGAGIVPASSPLGEWRETGVKLSTM
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                                                                                                                                           Similarity
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                                                                                                                                                                                          503 AA;
                                                                                                                                Conservative
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                                     ETMLQVSSVVMKLRNRSLG
                                                                                                                                                                               ; ~; 1.
A; 55359 MW;
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28.6%;
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                                                                                                                              Score 307.5; I
Pred. No. 8.6e:
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Last
Last
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Pred. No. 9
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Brassicales;
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                                                                                                                                                                       Query Match
Best Local S
Matches 106
                                                                                                                                                                                                                                                                         STRAIN-CV. COLUMBIA;

STRAIN-CV. COLUMBIA;

Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu Lee J.M., Liu X., Vaysberg M., Sakz Chin C., Chol E., Chiou J., Altafi H., Araujo R., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shin Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis , "Arabidopsis thaliana chromosome i BAC F25A4 sequence.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AC001765; AAF15941.1;

EMBL; AC001863; AAD55272.1;

EMBL; AC00863; AAD55272.1;
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Q9S7H8;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M. Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome I BAC FIM20 genomic sequence. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOCHORISMATE SYNTHASE (ICSI).
F1M20.39 OR F25A4.31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassicaceae;
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                                                                                     74
                                                                                                                            VEKALEMINQKSSPLNKVVLARNSRI-ITDTDIDPIAWLAQLQR---
                          TENLIDTL-AIDQTLAKVVFGRQQTLQLSDT----LRLAQITRALAEQANTYHVVLKRH
                                                                                   ELMAGFWFVPEVMVTIAADKITFGSDTVSDFTTWLAQFVPKQPNTVTTSHVTDEVDWIER
                                                                                                               AVEWEPFGAFYFSVPQVEFNEFGGSSMLAATIAWDDELSWTLENAIEALQ-
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                                                                                                                                                                                                                                                            PF00425;
                                                                                                                                                                                       Similarity
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(TrEMBLrel. 13,
(TrEMBLrel. 14,
                                                                                                                                                                       Conservative
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                                                         ETMLQVSSVVMKLRNRSLG
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lons; Rosidae;
                                                                                                                                                                         59;
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                                                                                                                                                                      Score 307.5; DB 1
Pred. No. 8.6e-16;
9; Mismatches 158
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; eurosids II;
                                                        -----VSVLSKNHVPTKGAYFPA
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EGHDAYQFCLQPP
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Sakano
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Best Local Similarity
Matches 108; Conser
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01-JAN-1999
01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mercado-Blanco J., Olsson P.E., van Loon L.C., Bakker P.A.H.M., "Analysis of a gene cluster involved in salicylate biosynthesis detection of a novel siderophore in Pseudomonas fluorescens WCS: Submitted (JAN-199) to the EMBL/GenBank/DDBJ databases. EMBL, Y09356; CAA70528.1; -
                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000350; -
PFAM; PF00425; chorismate_bind;
PRODOM; PD000779; -; 1.
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Bacteria; Proteobacteria;
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                                 EAALYYIATHEKTPRGLFAGPIGYFTADNSGEFVVGIRSMYVNQTQRRATLFAGAGIVAD
                                                                                                                                 FISATPERLVAMSGGQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASIT
SDAQQEYEETGLKFEPM
                      ERARRLIRFVEPFERGLFTGMVGWCDAQGNGEWVVTIRCGTVRRNKVR--LFAGAGIVEA
                                                                     SQLGKLCTQLNVPQRPSLISTPALWHLSTRIEGTLADPAVSALQLACRLHPTPAVCGFPT
                                                                                             TRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITGDIA-AHLSVTAIVDRLHPTPALGGVPR
                                                                                                                     LIGVSPELLVRKEGLSSLSNPLAGSAKRMADPEADRRNADWLLTSEKDHYEHGFVTQDIV
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                                                                                                                                                                                            QTLAKVVFG----
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Tremblrel.
Tremblrel.
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43102 MW;
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Last annotation updat
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RESULT
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Best Local S
Matches 78
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01-MAY-2000
01-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gloeckner G., Rosenthal A., Valentin K.;
"Reconstruction of the ancient red algal plast
gene repertoire, and synteny.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ
EMBL; AF022186; AAF12987.1;
INTERPOK) IPR000356;
PFAM; PF00425; chorismate_bind; 1.
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01-MAY-2000 (TrEMBLrel. 14, Laa
01-JUN-2000 (TrEMBLrel. 14, Laa
01-JUN-2000 (TrEMBLrel. 14, Laa
HYPOTHETICAL 52.3 KDA PROTEIN.
 "Pyrococcus abyssi genome structure and evolution.";
                                   STRAIN-ORSAY;
                                                                               Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 44
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                       Heilig R.;
                                              SEQUENCE FROM
                                                                                            PAB2045
                                                                                                      ANTHRANILATE
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                                                                                                                                                                                                                     NNFNTIIE
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78; Conserv
                                                                    Euryarchaeota;
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449 AA; 5
                                                                                                                (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                   (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 14, Last annotation update) SYNTHASE COMPONENT I (TRPE).
                                                                                                                                                             PRELIMINARY;
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52316 MW; B77
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14,
                                                                    Thermococcales;
           sequence:
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Last annotation updat
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No. 6.2e-15;
           insights
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                                                                   Thermococcaceae;
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           chromosome
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
PUTATIVE ANTHRANILATE SYNTHASE COMPONENT I.
INTERRO; IPR000350; -.
INTERRO; IPR000350; -.
PFAM; PF00425; chorismate_bind; 1.
PRINTS; PR00095; ANTSNTHASEI.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; UNKNOWN_1.
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INTERPRO; IPR000350; -.
PFAM; PF00425; chorismate_bind; 1.
PRINTS; PR00095; ANTSNTHASEI.
SEQUENCE 434 AA; 49058 MW; IFFBF19D48BD193C CRC64;
                                                                                                                                   Redenbach M., Kieser H.M., Denapaite D. Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detaile the 8 Mb Streptomyces coelicolor A3(2) Mol. Microbiol. 21:77-96(1996).
EMBL; AL096884; CAB51435.1; -.
INTERPRO; IPR000276; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
Seeger K.J.,
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
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Submitted (JU
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(JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                  (JUL-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J.,
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e EMBL/GenBank/DDBJ databa
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r A3(2) chromosome.
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1. No. 1.5e-11;
----ches 113;
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Best Local
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                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                 INTERPRO; IPRO00991; -.
INTERPRO; IPRO02385; -.
INTERPRO; IPRO02385; -.
PFAM; PF004725; Chorismate_bind; 1.
PFAM; PF00117; GATASE; 1.
PRINTS; PR00095; ANTSNTHASEI.
PRINTS; PR00096; GATASE.
PRINTS; PR00097; ANTSNTHASEII.
PROSITE; PS00442; GATASE_TYPE_I; 1
PRODOM; PD000779; -; 1
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01-FEB-1997
01-JUN-2000
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P72539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPA.
Streptomyces pristinaespiralis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4-dimethylamino-L-phenylalanine p
Mol. Microbiol. 23:191-202(1997).
EMBL; U60417; AAC44866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and analysis of genes from pristingespiralis encoding enzymes involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 97197164.
Blanc V., Gil P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO00350; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schleuniger J., Bisch Thibaut D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                     462
 205
                                                                        146
                                                                                                           402
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                                                                                                                                                                              Local Similarity nes 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12
                                                                                                                                           VSDFTTWLAQFVPKQPNTVTTSHVTDEVD------WIERTENLI---DTLAIDQ 145
GQIATAAVAGTSRRGTDGADDIALGEALLASQKNRIEHQYVVASITTRLQDVTT--SLKV
                                   TNMLRVPGR-----IDPLTAYRALRTVSPA--PYAAYLQFPGATVLSSSPERFLRIGAD
                                                     TLAKVVFGRQQTLQLSDTLRLAQIIRALAEQANTYHVVLKRHDELFISATPERLVAM-SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDTAIAIRTALL----RDGTAYVQAGAGVVADSDPVAEDTE
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                                                                                                       LTDAARTLATTAPRPPFTLLPDDQLPALDVHYRHSLPRYRELVEECRRLITDGETYEVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEFVVGIRSMYVNQTQRRATLF - - AGAGIVADSDAQQEYEE
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(TremBLrel. 02, Last seq
(TremBLrel. 14, Last ann
                                                                                                                                                                                Conservative
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                                                                                                                                                                                               10.9%;
25.7%;
                                                                                                                                                                                                                                                                       77363 MW; BFEBFCBDA91D8368 CRC64;
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i0; Mismatches 141;
                                                                                                                                                                                               Score 219; DB 2
Pred. No. 1e-08;
                                                                                                                                                                              Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Streptomyces
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Best Local Similarity
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                                                                                                                                                                      Q9X918 PRELIMINARY;
Q9X918;
01-NOV-1999 (TrEMBLrel. 12, Cr
01-NOV-1999 (TrEMBLrel. 12, La
01-MAY-2000 (TrEMBLrel. 13, La
SALICYLATE SYNTHETASE, IRP9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         094582;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-JUN-2000 (TrEMBLrel. 14, Last annotation
ANTHRANILATE SYNTHASE COMPONENT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
PRODOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyne M., Rajandream M.A., Barrel Submitted (OCT-1998) to the EMBL EMBL; AL031966; CAA21443.1; -. INTERPRO; IPRO00350; -. PFAM; PF00425; chorismate_bind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                094582
  SEQUENCE FROM N.A. Rakin A.V., Pelludat C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
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                                                                             Yersinia
                                                                                                       Bacteria;
                                                                                                                            Yersinia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VADSDAQQEYEET 379
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KVRAIQLYYGLEKEKRGIYAGAVGRWGYEDDNMDTCIAIRTMVYKDGT---VYLQAGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVSRVCDLDTT-SVDKLMTIEKFSHVQHLVSQVSGVLRPDKTRFDAFRSIFPAGTVSGSP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITTRLQDVTTSLKVPAMPSLLKNKQVQHLYTPITGDIAAHLSVTAIVDRLHPTPALGGVP 308
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Last sequence update)
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Pred. No. 6.2e-09;
15; Mismatches 84;
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Best Local S
Matches 86
                                                     Blattner F.R., Walsh C.T., Perry R.D.;
"Iron acquisition in plaque: modular lo
yersiniabactin by Yersinia pestis.";
Chem. Biol. 5:573-586(1998).
EMBL; ALO31866; CAA21385.1; -.
EMBL; AF091251. AAC69582.1; -.
INTERPRO; IPR000350; -.
PFAM; PF00425; Chorismate_bind; 1.
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01-MAY-1999 (TrEMBLrel. 1
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AJ132668; CAB46570.1; -
INTERROW, IPR000350; -
PFAM; PF00425; chorismate_bind; 1.
                                                                                                                                                                                                                                                                                                                           SPECIES=Y.PESTIS; STRAIN=KIM6+; MEDLINE; 99035519. Gehring A.M., DeMoll E., Fether Blatter F. B. Galle G. T. Formal Blatter F. Fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchrieser C., Rusniok C., Couve E., Frangeul L., Billault A
Kunst F., Carniel E., Glaser P.;
"DNA sequence of the 102 kbases unstable region of Yersinia
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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MW.
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Pred. No. 6.2e-09;
7; Mismatches 145;
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GAI-LLLDDTRFDAALVLRSVF--QDSQRCWIQAGAGIIAQSTPERELTET
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                                                   RQRGSVQHLGSGVSGQLAENKDAWDAFTVLFPSITASGIPKNAALNAIMQIEKTPRELYS
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